

CGGACGCGTGGGTGCCAGGCCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA
CCTGGTGCCACACCAACC**ATG**TGTGGCTGCAAGCGCTGGTGTGCTCCGGACACTACCTTCTAGG
GTTTTCACCAAGCTTTTCCAAGAACCTCCCTGTGTGAAGAATTCCATCAGCAAGAATCA
ATGGCTGTAAACACCTAGCAGGGAATATGCCACCAAAACAAGAAATGGGATCCGGCTGGGA
GAACCTGGCCAAAGAACTCAAAAGAGCGCAGCATTTGGAACCTCATGATGGAAAAAATATTAAAAAT
GATCAGATGGGAGAAGATGGTTTGTGCTGAGGGGGCTGCTGTTGGTCTTGGAGCATTTGTCTA
CTATGGCTTGGGACGTGCTCAATAGATTTGAGACTTGAAGCTATGAAAAGGCTGTAATTTGGCCTCAGT
ATGTCAAGATAGAATTCAATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
TTGTCTGCCATAGCAATCAGCAGAAGCGCTTGTCTCATGAACCTCATGATGAGAGGCTCTTG
GGTGACAATTTGGTGTGACCTTTGCAAGCCATGGTTTGGAGCTGGAATCTGCTGATCATCAATAC
CATATGACGAGAGCCCAAGGCCCAAAAGCATCTTGCTTGGTGTCTACATTCTGGTGTGATGGGT
GCAGTGGTGGCTCCCTTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGGTACAC
AGCTGGCATTTGGGAGGGCCTCTCCACTGTGGCCATGTGTGCGCCCAAGTAAAAATTTCTGA
ACATGGGTGCAACCCTGGGAGTGGGCTGGGCTCGCTCTTGTGTCTCATTTGGGATCTATG
TTTCTTCCACCTACCAACGCTGGCTGTGTGCCACTCTTTACTAGTGGAATGTACGGTGGATT
AGTCTCTTTTACGATGTTCTCTTCTGTATGATACCCAGAAGATCAATCAAGCGTGCAAGAGTAT
CACCATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
ACATTAATAATATATTTATCGAGTGTGCAACTATGCTGGCAACTGTGGAGGCAACAGAAAGAAATG
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAAATCTGTGTTAAATGGGCGAGATATGC
ATTAATATAGTTTGTACAAGCAGCTTTCTGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA
TTAAATGTTCCCGTAATGCTAGTCCCTCAGGCTCGCTCTTTTTCTGGGAATAAATGCAGT
AATCCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGGAGTGATTTTAAATGTT
TTGGTGAATGTGAAAACTAAAGTTGTGTGTCATGAAAGTGTAAGTCTTTTTTCTACTTTAAAA
TTTGTAGTGGTTTCACTGAGTAACTAAATTTAGCAAACTGTGTTTGCATCTTTTTTGGAGT
GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACAGAGAGAAG
GAGTCACCTGCGAGTCTTTGTTTGTTTTAAATACCTTAGAATAGCACTGTGTTGTTATTGATTA
GTGAGGAGCGCAGTAAGAAACATCTGGGTAATTTGGAACAAGTGGTCATTTGTACATTCAATTT
GCTGAGATCAACAAACATGTTTCATCTGAAACAGGCGACAGGTGATGCATTTCTCTGTGTTG
CTTCTCAGTGCTCTTCTTCCAATATAGATGTGTCATGTTTTCATTTGACAGAAATGTTAATC
ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTACAAAAGGAA
ATAACTTTTAAACATATTTCTACAGAGAAAATATTTCAAGCATGAAATATGTTGCTTTTTCCGAC
AATACAAACAGTATACATCAG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFWAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGIVLFSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIMDTLNI FMRVATMLATGGNRKK

099551.1401

AGAGCTGCTCTGCTCTGCGGAATTGGTGTCGGGACCTGCGGCCGCTCGCTGCTTCGATCA
 GGGCGCTTGGGCGGCTTCCACTAGACACCTAACAGCTCGGGAGCGCGCGCTGGTAGGG
 GGTTCGGCAGCGGGAGTCGGCGGGTCTTGTCATCTTTGGCTACTGTGGGTGCGAAATCGCTCGG
 ACATTCGGAGATGCTGCTCAGGAGCAATCCGGCGCATCCAGCGGCTATTGGTTCGCCGACCGCTG
 TCGGATGCTGCGGCAAACTCGGCCCTCATCGACCGCGGCTACCTCTCTCTCGGCCCA
 AGCCTTCCTTTTCGCTTTTCAGATTTCGAGGAGCAACATCATGCCACCTTTTATTTCCCTGTGG
 GTCCAGGAATCGATTTCCTTATTTGGTCAATTTATATTTCTTATCATAGTATTTACGCGA
 CTTGAAACAGGAGCTTTTAGGGAGGAGCCAGCATATTATTCATGCTCCTCTTTAACTG
 GATTTCATCTGTCGATTACTTGGCTTACGAATGGAATGATGCAATGCTGTATGATTCCTCTGATC
 TGTCACTATTTATGTCTTGGGCCAGCTGAACAGAGACATGATTTATATCTTTGGTTTGA
 ACAGCATTTAAGGCTCTGATTTTACCTCGGTTATGCTTGGATTCAACTATATCATTCGGAG
 TCGGTAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCCTAATGTTCA
 GATACCCCAATGGACTGGGAGGAGAAATTTTCTATCCACAACTCAGTTTGTTCACCGCTG
 CTGCCACCTAGTAGGAGGAGGAGTATCAGGATTTGGTGTGCCCTGTAGCATAGGCGAGC
 TGCTGATCAGAATTGGCGGAGCGGGAGACCAACTGGGGCGAGGGCTTTTCGACTTGGAGACC
 AGTGAAGGCGCGGCTCTGGGACCGGCTCTCTCAAGCCACATTTCTCCGACGTCTGGGTG
 CACTTTAACAACTCGCTTTCTGGTCAACATCTTGGACGTCACCCCAACTGAATGTAGTCTTTC
 AGTACGAGAGCAAAAGTTCTTAAATCCCGAAGAAAATAATAGTGTTCCCAAGTTTTCAGAT
 TCTCATCTCAAGTCTCTTACTGCTGTGAAGAACAATAACCAACTGTGCAAAATGCGAAATCTGAC
 TACATTTTGTGGTCTCTCTCTCTCTCCCTTTTCGCTGTGAATAAGGGTTTAGCGGGCTCT
 AATCTGCTGCGCATTTAGCTGGGGCTGGGTACCAAAACCTCTCCCAAAGGACCTTATCTCTT
 TCTTGACACATGCTCCTCTCTCCACITTTTCCCAACCCCACTTTGCAACTAGAAAAGTTGT
 CCCATAAAATTGCTCTGCCCTTGACAGGTTCTGTATTGTTATGACTTTTGTGCAAGCTGTGTC
 ACAACAACTATATTCAGTTATTTTCCCTTTTGGTGGCAGAACTGTATCAACTATGGGGAG
 AAGACAGCCACCGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTTCGACTGACATCGTGTGT
 AACCGTTTGGCACTCTTCAGATATTTTATATAAAAGTACCACTGAGTTCATGAGGGCCA
 CAGATTTGGTTATTAATAGATACGAGGGTTGGTGTGGTGTGTGTGTTCTCGAGCTAAGTGA
 TCAAGACTGTAGTGGAGTGCAGTAACTAATGGGTGAGTTTAAACCTAGGGGATGCACCCC
 TTTCGCTTTCATATGTAGCCCTACTCGCTTTGTGTAGCTGAGTAGTGGGTGTGCTTTGTGT
 TAGGAGGCTCCAGATCATGTGGCTACAGGAGAGTGCTCTCTTTGAGAGSTCTGGGCATGT
 ATTCOCATTTCAATCTCATCTTGGAATGTGTTCACTTGAATGAAGGAGGAGACGCCCTCAT
 CGCTATTTAAATGTCACTTTTTTGCCTATGCCCGGTTTTTGGTCATGTTCAATTAATGT
 GAGGAAGGCGGACGCTCTCTCTCGACGATGATCATTTTAAAGCTAATGTAGAGCACTAT
 AGGGAATAACATGATTTAAGTTTGAATGGCTTTAGAATCATTTGGGTTTGAGGGTGT
 TTTTGAAGTCATGAATGTACAAGCTCTGTGAATCAGACAGCAATAATTCAGCTCTTT
 TCGTATGTTGGGCTTTTCTATCAGAGTTGGCTCATAGATCAATTTTCAAGCTCTTT
 TGGCTTTTTCACAGATTTATTTATTTGAGTGTGTTGAGGAGCTTTTTCAGGCA
 TGGCTTTTTCACAGATTTATTTATTTGAGTGTGTTGAGGAGCTTTTTCAGGCA
 ATTGAGTGGGCTCAGACTTTTGTGACCAATAGGCTTTCAACGTTTGTAGCTGTTCTT
 TTTGAGTGTGAGTGAAGTGAAGTACTGACTATTTTCCCACTCTTAAACAGTGTGAT
 GTGTGTTATCTTAGAANAATGAGATTTGGCAACAACCTTCAATTTGAATAGAGTTTGTGT
 TACTTCTCATATTTAAATTTATGATAAAATGCTGGGAGACTTGAACCTTAACTGTCA
 TGTTTTGTGTTCTATCTGTGGCCACAATAAGTTTACTTGTAAATTTTAGAGGCCATTACT
 CCAATTTATGTTGACGTACACTATTGTACAGGCTGGAGACTCATTTGATGTATAGAATA
 TTTCTGACAGTGAGTGAAGCCGAGCTCTGTGTGTACCCCTTTTACAGCTCAGCTGCTCGGAG
 CAGTCATTTTCTCAAAGGTTTACAAGTATTAGAAGTTTTCAGTTTCAGGCGAAAAGTTTCT
 ATGAAGTTATTTCTTTAAACATGGTTAGGAAGCTGTAGACGTTATGTATTTTGTCTGGATT
 ATGTTTCTGGAATTAATTTTACCAAAACAGCTATTGTAGTTTGTACTTGAACAGGCAAAACA
 TGACAGTGGAATCTCTTTTCAAAATGAAAIAAAAAAATCCTTATTTGTATATAAGGACTCCC
 TTTTGTGAACAACTATCTTTTATTGTTGATAAAATGTAAATTTAAATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGKLPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGRFKACYLPWVILGFNYIIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFR
LDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAAGTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCCTACCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTGCGC
 CCTTTGGGGCGGG**ATG**GGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCTCGAGGCCAGACTGGTCCATCCCATCTTGGACTTGTGGAAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAAGTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTTCGAATAATTCAAGAGAGAAATGGTGATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGGAAGAGATGAAAAATCCT
 GAGGGAAGTCTTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
 AATAATTTCCCAAGGGGATGGTGAACATTTTGACACCCACCCCTCAGAAGTTAAAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAACTTCTCCCTCC
 CACAAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAC
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTTGCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAEEEEDEVWVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTIONPLAKTHTSQAILQP
VLAADFTIFKAMMVQKNIEMLQAIIRIIQERNVLPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTG
 TAGCTTCTCCACGTATGAGCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAGAAAC
 AGTGGAAATGGAAAAACAGTGTCTGATGCTATCTGTAATATGCTCCTTGTCAACAATGTATAC
 ATTCTGCTAGTGGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAAGCTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCCTGGAAGGAATTCTCTGATTCATGAAGTGGTCCATTCTCGCCT
 TTCTTTATTTCTCGATAAATTGATTGTCTTCTATGTCCTGTCTCTATCTTCAACAGGCATG
 GCTGTTATCTTCTCAAAATTTAGCATTATAACAACAGCTCTTCTATTCCAGGATAGTGTGAA
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACCTTTACAGCAACCTTGGCAGGACGTGGATTTTCATCACGATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTATTCTTCAATGGCT
 AATATCTATAATGAAGAAGTACTGAAGGAGGGGAACAGCTCATGAAAGACTCTTCAATACA
 GAACAGCAAACTCTATTCTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCTCTCAGAGGA
 GTAACCGTGATCAGATTAGAAGCTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTTGTAAGTGCATTCCAGGGGCTTTTCAGTGGCTTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGTCTTGATGGCCAGGTTACCAGTCTATTATCACACAGTGTCTGTCTCTG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCATCAGTCTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCTCAAGTTCGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAAACCAAGAGTGATGAGTCAGATGAAGTACTTTCTAACTGGTACCACATAGTTTGCA
 GCTCTCTTGAACCTTATTTTACATTTTCAGTGTTTGAATATTTATCTTTTCACTTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATTCTTGGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCAAAAAAAGCTGTGAATAATCATGTTAGCTATAGCTTGTATAT
 ACATCATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAGT
 CTCTCCCTTTTAAACATTTAAAGAGCTAGGTTGCTCTTGAATTTTGGGCCCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCCCTTTCTAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTTTGGGATGATGAGTCTGTGCTAAATATTTTGTGGAAGAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGGAAATTTGGATTTTTGT
 AATAATCTTTTGATGTTTAAACATTGGTTCCCTAGTACCATTAGTACCAGTGTGATTTTAA
 AGTCATTTAAACAAGCCAGGCTGGGCTTTTTTCTCCTCAGTTTGGAGGAGAAAATCTTGAT
 GTCATTTACTCCTGAATTATTACATTTTGGAGAATAAGAGGGGATTTTATTTTATTAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTCAGATCATAC
 CAGATTGTGAGTGAAGCTGATGCCTAGGAACCTTTAAGGGATCCTTTCAAAGGATCACTT
 AGCAAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAATAGAAAAGAC
 AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGTGATGGTATTTTCTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
 AAATAGCAAAACAAAGTGACTTGCTCAGGGTATCGAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGGCTGTATGTTTACAGACTACCATCTGTAAGTATGAGCTTTATGGTGT
 CATTTCTCAGAACTTATACATTTCTGCTCTCCTTCTCCTAAGTTTCATGCAGATGAATATA
 AGTAAATATACTAATTATATAATTCATTGTGATATCCCAATAATATGACTGGCAAGAATTG
 GTGGAATTTGTAATTAATAATATTATAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
 IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIIITVSVLVFDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTTPKPSDEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAAACAGTGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACCAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCAATCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCCTGATTTTCATGAAGTGGTCCATTCCTGCCTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC
TGGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCGAGCGCCTCGCGGGCAGGAGGACAT
CCGCTCTACAGGTCCTCAAGCGCGCTGGCCCGGGGTATGCGCAAGGAGAGGCGCCGAG
AGCGGCTCCGCGGCGGGGCTGCTACCCACGAGCATCTCCAAAGCATGAAGCCCGGCCCA
GGTGAAGAAAGACCCAAAAGAAAGAACACAGTTGTCTGTTTGCACAAAGCTTTGCTATG
CACTTGGGGAGCCCTTACAGGTGACGGGCTGTGCCCTGGGTTTCTTCTTCAGATCTA
CTATTGATGCTTGGCTCAGGTGGGCCCTTTCTCTGCTCCATCATCTGTTTGTGGGCGGAG
CTGGGATGGCATACAGACCCCTGTGGGCTTGTGATCAGAAATCCCTCGACCTGCC
TGGGTGCGCTTATGCCCCTGGATCATCTTCTCCACGCCCTTGGCCGTCAATTGCTACTTCTC
ATCTGTTCTGTGCGCGCACTTCCACACGGCCGAGCACTTGTGACTCTGCTTTCTATTGGCT
CTTTGAAACAATGGTCACTGTTTCTTCACTGTTCCTACTCGGCTCTACCAATGTCATCAGCA
ACCGAGCAGACTGAGCGGGATTCTGCCACGCCCTATCGGATGACTGTGGAAGCTGCTGGGCAC
AGTGTGGGACGCGCATCCAGGACAAATCTGGTGGCCCAAGCAGCGCTTGTTCACGAG
ACTTCAATAGGCTCTACAGTAGCTTCAAAAGTGGCCACCATACATAGTGGACCACTTCACAC
AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGTATTGCTGTGATATATATAATCTG
TGCTGTCACTGTATCCTGGCGTGGGAGCAGAGAACCCTATGAAGCCGACGAGTCTG
AGCCAATCGGCTACTTCCGGGGCCTACGGCTGGTCTAGGCCACGGGCCATACATCAAATCT
ATTACTGGCTTCTCTTCACTCTCTTGGCTTTTATGCTGGTGGAGGGAATTTGTTCTGTT
TTGCACTTACCTTTGGGCTTCGCAATGAATTCAGAACTACTCTTGGCATGCTCTCT
CGGCCACTTTAACCATTTCCATCTGGCAGTGGTTCTTGACCGGTTTGGCAAGACAGCACT
GTATATGTTGGGATCTCATCAGCACTGCCATTTCTCATCTTGGTGGCCCTATGGAGAGTAA
CCTCATTTACATACATGCGGTAGCTGTGGACGCTGGCATCAGTGTGGCAGCTGCTCTTTAC
TACCCTGGTCCATGCTGCTGATGTATTGACGACTTCATCTGAAGCAGCCCACTTCAT
GGAACCGACGCCATCTTCTTCTTCTTATGCTCTTCTTCAACAGTTTGGCTTGGAGTGTC
ACTGGGCATTTTCTACCCTCAGTCTGGACTTTGCAAGGATACGACCCGTGGCTGCTCGCAGC
CGGAACGCTGTCAAGTTTACATGAACTGCTGTCGACCATGCGTCCCATAGTTCTCATCCTG
CTGGCGCTGCTGCTCTTCAAAATGTACCCCATGATGAGGAGGCGCGCGGCAAGTAAGAA
GGCCCTGCAAGGCACTGAGGGACGAGGCCAGCAGCTGTGGCTGCTCAGAAACAGACTCCACAG
AGCTGGGTAGCATCTCTCTAGGCGCGCCGACGTTGCCGAAGCCCACTGCAAGAGGCCACAG
AAGGATAGCAGGACTGTCTCGCGGCTTGTGTAGACAGCTGGACTGACGTTGCTAGGAAGGAA
CTGAAGACTCAAGGAGGTGGCCGAGACATCTGGTGTGCTCACTGTGGGCGCGCTGCTCTG
TGGCCTCTGCTCCCTCTGCTGCTGCTGGGCTGAGCCAGCCCTGGGCTGCCATCTGTAAT
TGCCAAGGACTGATGGGCGCTAGCCCGGAACACTTAATGTAGAAACCTTTTTTTTACAGGCC
TAATTAATAACTTAATGACTGTGATACGATCAAGTAATGTGTGATGTATGTATGTGAGCTA
TTAATGTTTATTAATTTTCTATAAAGCTGGAAAGC

MWLRWALSILPSSSCLWAEFGMPSQTPWWASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHRTARPIGTCFSIASLKQWSRVSMFTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGGQIVGQADTPCFQDFNSSTVASQSANHTGHTTSHRETKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAAQQSEPIAYFRGLRLVMSHGPIYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGRNEFQNLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYASVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFTTKFASGVSLG
ISTLSDLFAGYQTRGCSQPERVKFTLNLMLVTMAPIVLILGLLLFKMYPIDERRRKNKKAL
QALRDEASSSGCSETDTSASIL

FIGURE 13

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGCTACTTGAATACTGAGTTGTTTAGG
 ACTTTCATTGTGGCAAACCTCCAGAAAACAACCCTTTTGTCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
 CAGCCCAAATCCATGGCAAACAAGTCTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTCACTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAAATCCATTGGAACCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAAATGGTCTATGTCAATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAAACCCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAGAAGCCATTTGATAGATTATTTCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACCTATGCCTATACTTTTTATCTCAGAAAAATAAGTCAAAAGACTATG

MWWFQQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATYVRYRQVHALSPEENVIKLNKAGLVGLISCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSVLHSGNFG
TDLEQKLHWNPNDEKGYVLHMITTAEEWSMSFSFFGFFLTYYIRDFQKILSRVEANLHGLTLYD
TAPCPINNERTLLSRDI

FIGURE 16

CGGACGCTTGCGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTGTTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCCAAAAAGCTAATTGAGTACACGTTCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTA AAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

CCACGCGTCCGCCCGCGCTGCTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG
CCGGGGTGCAGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC
CTTCGCCTTGTACTTGTCTGTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
AGGCTGGAGGCAGGTGCTGTGGTTCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCACGTGTTCCTGCTCTTCTGCGGCCTCA
CCTCTACAAACAGGGCTTTGCCATCCCGGCTCCAGCTTCTGTAATGTTTTAGCTGGTGCCT
TGTTTGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC
TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT
GGCCTGCTGCAGAGAAAGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
TGAGACTTTTCCCATGACACAAACTGGTTCTTGAACCTCTCGGCCCAATTCTGAAACATT
CCCATCGTGCAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCACTGTGT
GCAGACAGGGTCCATCCTGTCAACCTTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCTCATTAATAAATTT
AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAAGA
CACATGATCTGGATTCTGTGTTGCCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA
TGTGTCCTCTAAAGCCCTCATTTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
TTTCAAACCAGCCCTGGTGTAGCAGACATGCAACAGATGCCTCCTAGAAAAATGCTGTTGT
GGCCGGGCGCGGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATT
ACAAGGTGAGGATTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGCTCTTAATAAAAAAT
ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAATGAGCCAAGATCACACCAGTGCAT
CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
KEHQAYVFLFLFCGAYLYKQGFAPCGSSFLNVLAGALFGPWLGLLCCVLTSTVGATCCYLLSS
IFGKQLVVSYPDPKVALLRKVEENRNSLFFFLFLRLFPMPTPNWFNLNSAPILNIPVQFF
FSLVLIGLIPYNFICVQGTLSLSTLSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
LNLETSTANHIIHSRKDT

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31.

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCGAGGGGCGCGAGCCCGCATGAATCATTTGTAGTCAATCATTTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGACACGTGGTTTCCGAACAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
 TTATGACAAACTTTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
 CCCCCGCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTAGCCCCATTAGCACCTGAGCCAGTGCCTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGTGATGAAGACAGACCTTTT
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCATTCTTGCC
 AACTGCAGTGGCTGTGCCAGAAACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCCTGAGGCGCAGAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCTGAGCGGTGGTTCCTTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCAGAAATGTTACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTCAACCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCTTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAAGTCTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAA

MDLAANEISIDYDKLSETVDLVRQGTGHQCGMSEKAEIKFIRQLLEKNEFQRPPFPQYPLLI VVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHTRLMSLP IAKYMSENKGVPL
HGGDEDRPFPDFDFPWWTNDCEQNESEPI PANCTGCAQKHLKVMLLEDAPKRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEPGVSEGGFAKWWRCFERWFFPPYPWRRLNRSQMLRELFPV
FTHLFPKYDASLNKCSFLHPETFGVSGMKMHKMDLFI ISGSEAMLQI LPPFQCRRHQCSVAMP
IEPGDIGYDSTTHWKVYVIARGVQLPVLICGTAFSEL

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAACCTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTGAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATCAAC
CTTTCAGCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGGCTCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGT
 CCAGTGGTGCACAGCTGCTAGACCGTGCCTATGAGCGCTGGGGCTGCAGTGGGGACTGCC
 CTCCTGCCACCAATGGCAGCCCACTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA
 CACCCGAATGGCGCACTTATCGACAAACAGGTACAGCCAACTAGGCTCCAGATTGCAATG
 GACACGCTATGTCTAAGAGCCAGCACTTATGTACGTTTCTGGAATGCTCTATGACATGTCT
 TATGAGCAGTGGGACGCGGCCAGTGGAGCGCGCCAGAGTCTCGGGGCTTCCAGGAGC
 TGGTGTCTGGAACCTGCGCAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGCTG
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCATGGGGGGCGCTGTGGCGGAGCT
 CGCCAGCCATGTGGGGCTGGCGCTGAGGGACACTCCCATCCCCCGCTGGAACCTGTCCA
 GCGCGAGACATATTACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAACTCTGGGTGAGGTTCCCTGACACCCACGAGGAGGC
 CTCACCTGCTCTGGCAGTGACCAAAGAGGCCAAAGTAGCACCACCCGAGTTGCTCGAGG
 AGGACCAGCTCGGGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCAGCAGAATCTG
 GATGAGCAGCGTGAGAAGCTGGTGCTGTGCGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCAGGGCTGCTGGAGGTCAACACAGAATGTATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAAAGCCAGGAGGGCTCGGCTATGATTTTCCGCGCCCACTGGCCAGCTGCGTGAG
 TCCACCTGCGGCGTTTCAAGCTGCGCGCTTACGACCTTGAGCTCTTCTTATCGATCAGGC
 CACTACTTCTCAACTTCCCATGCAAGTGGGCAGCACCAGCTCTACTCTCCATGCCAGCA
 CTCGAGAACCCAGCTGGCGCCATCCACCCCATACCAGGTACGGAACCAAGGTGTACTCG
 TGCTCTGCGGCTACGGCCCTCTCAAGGCTTACCTAAGCAGCGCTCCCCAGGAGAT
 CTTGCGTGGCTCAGGCCCTTACCAGAAATGGGTACAGGCTGAGATATCAACTTCTCGAGTACT
 TGATGCAACTCAACACCAATTCGCGGGCGGACCTACAATGACCTGTCTCAGTACCTGTGTT
 CCTGGTCTCTCGAGGACTACGTGTCCCCAACCTGGACCTCAGCAACCCAGCGCTCTCCG
 GGACCTCTTAAGCGCTACGGTGTGGTGACCCCAAGCATGCCAGCTCGTGAGGGAGAATG
 ATGAAAGCTTTGAGGACCCAGCAGGGACCAATTGACAAGTTTCACTATGGCAACCCACTCTCC
 AATGCAGCAGCGCTATGCACTACCTCATCCGCTGGAGCCCTTCACTCCCTGCACTACTCC
 GTTCCAAAGTGGCGCTTTGACTGCTCCGACCGGCGAGTTCACCTCGTGCGGGAGCTGGC
 AGGCACGCTGGAGAGCCTGCCGATGTGAAGGAGCTCATCCGGAATTTCTTCACTTTCTCT
 GACTTCTGAGAACCCAGAACGGTTTGACTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTGCTTACCCCTGGGCGAGCTCTCTGAGGACTTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCTGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCCGCGAGGAGGCCCTCAATGTCTTCTATTACTGACCTATGA
 GGGGGCTGTAGACTCGGACCTGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATT
 TCAGCAACTTTGGGCAGACTCCTGTGACGTGCTGAAGGAGCCACATCCAACCTCGGCTCA
 GCTGAGGAAGCAGGCCATCGCCTTGACGCTGGACACTAATCACTAGCATCTTCCAGCA
 CCTGGAGCAACTCAAGGCATTTCTCGCAGAGGTGACTGTGAGTGGCAGTGGGCTGTGGGCA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCACTACTTGAGCTTCAGCAAGAGCCCC
 ACCATGGGAGCCCAAGACGACGACTGCTGAGTGGCCGCTGGGTGCCAGGAGTGGTGT
 GATGTGGACAAGCACTGGCAGTGGCCCGGATGGAAGCTGCTATTCAAGCGGTGGCCACTGGG
 ATGGCAGTGGCGGTGACTGCACTACCCGCTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGTATGTAGTAACCTGCTTGCACTGGACACTGTGGCATCTACCTCATCTCAGGCTGCCG
 GGACACCACTGACATGGTGTGGCGGCTCCTGCATCAGGTTGGTCTGTCACTAGGCGCTGGC
 CAAAGCTGTGCAAGTCTGTATGGGCATGGGGCTGCAGTGAAGTGTGTGGCCATCAGCACT
 GAACCTGACCTGTGTCTGAGTCTGAGTATGGAAGTGTGATACACACTGTACGCGG
 CGGACAGTTTGTAGGCGCACTACGGCTCTGGGTGCCACATTCCCTGGACCTATTTTCCACC
 TGGCATTTGGGTCCGAAGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACCTCTGGGGG
 CAGGTCACTACTCTTGCACTGTATTGAGTCAATGGGAAGTTGGGGGCTCACTGCCCT
 GGCAGAGCAGCTCAGCGCTGACGGTGACAGGAGCTTTGTGTTGCTGGGCACCGCCAGT
 GCGCCCTGACATCTCCAAGCTAAACACACTGCTCCCGCGCGCGCTCCTTGTGCCATGGAAG
 GTGGCCATCCGACAGCTGGCCGTGACCAAGGAGCGCAGCCAGTGGTGGTGGGCTGGAGGA
 TGGAAGCTGTGGCGGTCTCGCGCGCATCTCCAGGTTCTCTCGGAGAGACGGAATAACAAC
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGTGTCTGGGCGCGCGCCCGGCGAGCGCT
 GCGCGGAGGCGCGCGGAGAGTGGCGGGGAACCCCGGGTGGGCAACCCAGGGGGTGA
 GCGGGGCCACCTGCCAGCTCAGGAGTTGGCGGGCGATGTTACCCCTCAGGGATTGGCG
 GCGGGAAGTCCCGCCCTCGCGGCTGAGGGCGCGCTGAGGGCCAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMSSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRCLKLPN
 HHFDPHLEASALRDNLGCVPLTPTEEASLPLAVTKEAKVSTPELLQEDQLGEDELALETFP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLELVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPQTTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSP TLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEFFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESADVKELIP
 EFFFYFPDFLENQNGFDLGLCLQLTNEKVGDDVLPWPASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEEEALNVFYICYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSABEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTRQLLSGPPWVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIIYLISGSRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAS
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA
 WERPGAQVTVSYSLHYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLDGLIVVAGQPSEVRSSQFARKLWRRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCACCTTGTGAACCTCTGTCGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCAT
 CCAAAGCCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTC
 TGGACCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCAGGACATCCCTACCTTCCCTTAACTCTGCGCTCATCC
 GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGTGCTCTGGTGTCTGGAAAAATTTATCAAGTTC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTGTCTGAGCAAAAGTACAGA
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGCGCTGGGGGTCTGTCTCTTTT
 TTTCTCCGCTCGCATCCCGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGTGCCCATCATGACCTCCATCCTGGGGGCCTATGTCATCGCCAGCGGCTTCTTCAGCGT
 TTTCGGCATGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGTGAAACCTCC
 GTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTGATCCAGCTAC
 TCGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTGTCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAAACAA
 AAAGATTTATTAAAGATATTTTGTTAACTC

RTRGTRTGGCKEVPINTSCNPHTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNQLIYGVGLGF
WTLNWNVLALGQCVLAGAFASYWAFHKPQDIPTEPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLGRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGNFCVSAK
NAFMLLMRNIVRVVVLDKVTDLLFFGKGLLVVGGVGVLSFFFFSGRIPLGKDFKSPHLNYY
WLPIMTSLGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLLIKLGKN
EAPPDNKKAY

FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGTTACCTCAGCGGAGCGCCAGGCGTCCGGCCGCCGT
 GGCTATGTTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT
 CAGTGTGACCAAGTGAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAAGTGAAGTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCATGTATACAACGATACCCAGATCAAATTACTCATTAACAAGATGA
 TGACCTTGAAGTTCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGTCAGCG
 CCACGTTTCCCGCCACAACACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCTGGTGTCTACACGACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGAGTTCTTTGAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCTGCAGACTTTCAGCATTCATTTTGGGTTCAAGCACAAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCTGGAACTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATGCCAGCTGC
 CTTTGCACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCTTTGTGTGTTGACAAAGAACCAGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTGGGAGGGCGTTTGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCAACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCATTTATTTCCCTCCTGTCTTAGGAATTTGATTCTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCATTATGATTGAAGTTATGGACATGATTGAGATGTAGAAGCCATT
 TTTTATTAAATAAATGCTTATTTTAGGAAA

MFVSDFRKEFYEVVQSRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETA
LEHKEQFHYFILNCGANVDLLDILQPEDTIFVCDSHRPVNVVNVYNDQIKLLIKQDD
LEVPAYEDIFRDEEDEEHSGNSDSESEKTRLEEEIVEQTMRRRRRREWEARRRDLF
DYEQYEHGTSSAMVMFELAWMSKDLNDMLWWAIVGLTDQWQDKITQMKYVTDVGVLRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWLSHDSLNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKFQAMDISKENLREMIEESANKFGMKMDRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGFPLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNNHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGAATATANGCT
GGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCAGTACCATTTTTTCTAGTGAAC
 CACGAAGGGACGATACCAGAAACACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAGAGACAGTTTTTTTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTACAGCTTTTAACAAAT
 GAGTAAAGTACGTTCCGGTCACCAATGGTGACAGCCGCCCTGGTCCCCTCTGGGACGGCTC
 CTGCTCTTTCTCCATGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAGCGCTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCTCCAG
 CCTCTTCTCTCCGGCCGCCCCACGCCCTGCTGAGATCAGACCTACATTAAATATCACCATC
 CTGAAGSGTGACAAGGGGGACCCAGGCCAATGGGCCCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG
 GCGCCCGTGCCAGAAGCGCTTCTTCGCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC
 GGCAGGACTTCCAGAGCTGCTCTTCGAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCCACCGCCAGTTTGTCTGCCCTGCTGGCATCTACTTCTTCAGCCTCAATGTGC
 ACAGCTCGAAATACAAGGAGAGCTACCTGCACATTATGCATAACAGAAAGAGGCTGTCATC
 CTCTACGGCGCAGCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGAGGACCGCTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAAGCCATCTACAGCA
 ACGACTTCGACACCTACATCACTTCAAGCGCCACTCATCAAGGCCGAGGACGAGTCAAGGG
 CCTCTGGGCCACCTCTCCGGCTGGAGAGCTCAGGTGCTGGTCCCCTGCCCTCGAGGGCTCAG
 TTTGCACTGCTCTGAACAGGAAGCCAGGGAGTCCCCGGGAGCTCCGCTATCTGGGGAGA
 CCGTCTCTCTATCTTGGCTGCCATCATCCCTCCAGGCTATTCTGCTCTCTCTCTCTCTCT
 TGGACCTATTTTAAAGACCTTGCTAACTTAAATATTCTAGAATTTCCAGCCTCGTAGGCC
 AGCACTTCTCAAATTTGAAATGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCT
 GACTCAGCAGCTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTG
 ATGGGCTCAGTCTATGAACCACTGGAGCAACCAAGGTTCTAGGACTTTCTCAATATTCTAG
 TACTTCTGAACATTTCTGGAATCTCCCCACATTTCTAGAATTTCCCAAGCTTTTTTTTCT
 TGAGACAGTCTTGTCTGTTGCCAGGCTAGAGTGCAGTGGTGCATCTCAGTTCACTGC
 AACCTCTGCTCTCCGGGTTCAAGCATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGCGGCTGCTACCATGCTGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTACCATA
 TTGGCCAGGCTGGTCTTGAACCTCTGACTCAGGTGACCCACCGCTCGGCCCTCAAAAT
 GCTGGGATACAGGTGTGAGCCACCGTGCCTGGCCAATTCCAACATTTCTTAAATTTCTCTAT
 CCTCCAGGCTCCCCGTGCTATGTTCTCTTTACCCCTTCCCCCTCTTCTGCTCAGGCC
 TGCACCATGACCCACCGTTCAATTATTCAATTAACACTGAGCACTCACTCTGTGCT
 GGTCCCGGAAGGGTGAGGGGTGAGAGCCAGGCCCTGCCCTGCCCTCAGTCACTGGCCA
 GTCCAGCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCAGAGCTCTGGGG
 GCTGTGTTCTTGGGTGTTCAAGTGCTGCTGGTCTCCATTACCACCTGCTCCCCAAGGCTGG
 TGGGACGGGTCCTGGTGGCAGGGGCAAGTATCTCCTTCCCCTTCTCTATCCACCTGCCCGG
 TGCTCATCGTTACAGCAACCCAGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGCATTTGGGGGGTGAAGTGGCCCCGAGGAATGGAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCTGCGAGAAGACCTGAGGCTCTCTCACTGGGATCCC
 GTTCTCTGCTCTCTCCAGGGCTCTGCCAGGGCTTGGTCACTGCTCTCCACCAAGTCACT
 GAACCTCGCTTCTCCAGGGCTCTCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCT
 CTCTAGCCCTCATGCCCCCTCACCGGCCAGTCCCCGACTCTCCAGGCTTTATCAAGGTG
 CTAAGGCCGGGTGGGCGCTCTGCTCTCAGAGCCCTCTCCGGCTGGTGCTGCTTTTAC
 AAACACCTCAGGAGAAGGGGCCAGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTTCTGGGG
 AGCTACAGCAAGAGGGGACCTCAGGCCCTTCCGTTTCTTCTCAGAGGTTGGGTGGGCTGGT
 GTTCCCTAGGCTTCCAACCCAGGTGGCCTGCCCTTCTCCCCAGAGGGAGGCGGCCCTCCGC
 CCATTGGTCTCATGCAACTCTGGGCTGAGGTGCCCGGGGGGTGATCTCTGGTGTCTCAC
 AGGCCAGGGAGCGGTGGCTCCATGGCCAGATGACGGAACAGGGTCTGACCAAGTGCCAGGA
 AGACCTGTGCTATAAACACCCCTGCTGATCCTGCCCTGCTGACCCGCCAGGCCCTGGC
 GTCCAGCATGATTAAAGATGCTGTCTCCTCTTGGAAAAAAGAAAAA

0992521.11401

FIGURE 30

MVTAALGPVWAAALLFLLMCEIRMVELTFDRAVASGCQRCCDSEDLDPAHVSSASSSGRPH
ALPERPYINIITLKGDKGDPGMPGLPGYMGREGPQGEFGPGQSGKDGKMGSPGAPCQKR
FAFSVGRKTALHSGEDFQTLLFERVFNVLGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMSQSVMLDLAYGDRVVRLEFKRQRENAIYSNDFTYIT
FSGHLIKAEADD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAAGCAGTTGGCTTCGGGACCCAGGACCCCTCGGGCCGACCCGCCAGGAAAGACTG
 AGGCCGCGGCTGCCCGCCCGGCTCCCTGCGCCGCCCGCCCTCCGGGACAGAA**CATG**TG
 CTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGCCCCGGGGCCTGGGGTGCAGG
 GCTGCCCATCCGGTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCAGGGG
 ACCACGGTGCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAGCTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCCCTGCAGCTCCTGGACCTGTAC
 AGAACAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCAACAGGCTGCATGAAATCACCAATGAGACCTTCCGTGGCCTGCCGGCCCT
 CGAGCGCCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC
 TCGACCGCCTCTGGAGCTCAAGCTGCAGGACAACAGAGCTGCGGGCACTGCCCGCGCTGCGC
 CTGCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAAC
 CCGCATTGCCAGCTGCGGCCGAGGACCTTGGCCGCCCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTAAGCCTGAGGCCCTGCCTGGCAGCTCTCGGGCCTCTTCCCGCCTGCGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCACTGCGTGTGCCCTGAGCTGGTTGTGGCCCTG
 GGTGCGCGAGGACAGTGCACACTGCACCTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCA
 AGAACCTGCGCGCTGCTCCTGGAGCTTGACTACGCGCACTTTGGCTGCCCGACCAAC
 ACCACAGCCACAGTGCCTGCCACGAGGCCCGTGGTGCAGGCCCAAGCCTGTCTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCGGCCACTGAGGCCCCAGCCCGCCTCCA
 CTGCCCCACGCACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCCAACCGTCCACCTGCCTC
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGTGTGCCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCAAGTCA
 CGCCGAGGCCACACGGTCCCTGACCTTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACACGGTACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGG
 CCGGGCGGCTGCCGGAGGGCGAGGAGGCTGCGGGGAGGCCATACACCCCAAGCGCTCCA
 CTCCAACACGCCCCAGTCAACCAGGCCCGGAGGGCAACCTGCCGCTCCTCATTCGCGCCG
 CCTTGCCCGGCTGCTCTGGCCGCGCTGGCTGCGGTGGGGGACAGCCTACTGTGTGCGCGG
 GGGCGGGCCTGAGGACAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGCTGGGCCCTG
 GAACTGGAGGGAGTGAAGGTCCCTTGAGGCCAGGCCCGAAGGCCAACAGAGGGCGGTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTC
 CAGTCACCCCCTCCAGCAAGGCCCTACAT**TAAG**CCAGAGAGAGACAGGGCAGCTGGGGCCG
 GGCTCGCCAGTGAAGTGGCCAGCCCCCTCCTGCTGCCACACACAGCTAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGACGGG
 GGCCTGCCATGTGCTGTAAACGCATGCCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA
 CCTTGGGGCAGCTGAAGGAAGCTCCCGAAAGAGCAGAGGAGAGCGGGTAGCGGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTCCCATTTATCTG
 GGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTGAACACAACGATGATATG
 AAGGCCTTTTGTAGAAAAAATAAAGATGAAGTGTGAA

FIGURE 32

MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVFEN
GITMLDAGSFAGLPGLQLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRILELKLQDNELRALPPLRLPRLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNSLQALPGDLSGLFPRLRLAAARNPFNCVCLSWFG
PWVRESHVTLASPEETRCHFPKPNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPSTAPPTVGFVPQPDCCPSTCLNGGTCHLGRHHLACLCPE
GFTGLYCESQMGQTRPSPTPVTPRPPRSLTGIEPVSPTSRLVGLQRYLQGSSVQLRSLRL
TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVRGRAMAAAAQDKGVGPGAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPHLAKPYI

000001-1101

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATTCATTATATGAGGAATAAGTGGTAAAAATCCTTGGAAAAATCAATGAGACTCATCAG
 AAACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAGGGGAACTGATGACCAACTGCTCCAACATGCTCTCAAGAAAGGTTCCCGCAGACTGTG
 ACCCAAGCCACAACGACATGGATTATCTATAACCTCCTTTTCAACTCCAGAGTTGAGA
 TTTTCATTCTGTCTCCAAACTGAGAGTTTTGATTTCTATGCCATAACAGAAATCAACAGCTGG
 ATCTCAAACTTTGAATTCACAAGGAGTTAAGATATTTAGATTGTCTAATAACAGACTG
 AAGAGTGTATCTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT
 TGACACCATGCTTCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA
 TTCTTAGGATTGAGAATCTTCTCATTATGAAGAAGGTAGCTGCCCATCTTAAACACAAC
 AAACTGACATTTGTTTACCATGGACAAAATTTCTGGGTTCTTTTGCCTGATGGAATCA
 AGACTCAAAAATATTAGAAATGACAAAATATAGATGGCAAAAGCCAAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTAAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTTGGCATACATCAGTGGAACT
 TTCAGATCGGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC
 TCAGAACTCTAATGAGACATATAAAATGGAGCATGTACATTTAGAGTGTTTTACATTTCA
 ACAGAGATAAATCTATTGCTTTTGACCAAAATGGACATGAAAACTGACAAATCAAAATG
 CACAATGGCACACATGCTTTTCCCGAATTATCCTACGAAATTCCAATTTTAAATTTTGGC
 AATAATATCTTAAACAGACGAGTTGTTTAAAAAGACTATCCAATCGCTCACTTGAAACTCT
 CATTTTGAATGGCATATAACTGGAGACCTTTCTTTAGTAAGTTGCTTTGTCTAACACACAC
 CTTCTGGAACCTTGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAATTTGCTCA
 TGGCCGAACTGGGTCATATGAATCTGTCTACATAAATTTGCTGATTTCTGTTCTCAG
 TGCTTTGCCCAAAGTATTCAAATCTTGACCTAAATTAATAACCAAAATCCAACTGTACCTTA
 AAGAGACTATTCATCTGATGGCTTACGAGAATTAATTTGACATTAATTTTCTAAGTGAT
 CTCCCTCGATGCATCTTTTCACTAGACTTTCAGTTCTGAACATTGAAATGAACCTTCATTCT
 CAGCCCATCTCTGGATTTTGTCTCAGAGCTGCCAGGAAGTTAAACTCTAAATGCCGGAAGAA
 ATCCATTCGCGGTGTAACCTGTGTAATAAAAATTTCAATCAGCTTGAACATATTCAGAGGTC
 ATGATGGTGGATGGTCAGATTATACACCTGTGAATACCTTTAAACCTAAGGGGAACTAG
 GTTAAAAAGACGTTTCACTCCACGAATATCTTGAACACAGCTCTGTTGATTTGCACCAATG
 TGGTTATATGCTAGTTCTGGGGTTGGCTGTGGCTTCTGCTGCCATTTGATCTGCC
 TGGTATCTCAGGATCTAGGTCAATGCACACAAACATGGCACAGGTTAGGAAAAACAACCCA
 AGAACAACTCAAGAGAAATGTCGATTCACGCAATTTATTTATACAGTGAACATGATTTCTC
 TGTGGGTGAAGAATGAATGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTTGC
 TTTTATGAAAGCTACTTTTGACCTGGCAAAAGCATTAGTGAAATTTGTAAAGCTTCATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATCTACTTTTGCCCAACCAATCTCTCCATGAAAATCTGTGATCATATAATTTCTATC
 TTTACTGGAACCCATCCATCTTATGCAATTTCCACAGGATCATAACTGAAAAGCTCTGCT
 GGAAAAAAGCATACTTTGGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCCAA
 ACCTTCCAGCTGCTATTATGTTAATGTATGTATAGCCACAGAGAATGTATGACTGCAGACA
 TTTACAGAGTTAATGAAGAGTCTCGAGGTTCTACAATCTCTGATGAGAACAGATTTGTCT
 ATAAATCCCCACAGTCCCTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTTGATA
 CAACCTTTATGATGGCAATTTGACAATATTTATTAATAAATAAAATTTGTTATTTCCCTCATTA
 TCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAAACACCTTACAAGTTTATAAAG
 CGTTTATGGAAAAAGGTGTTTCAATCCAGGATTTGTTATATCATGAAAATGTGGCCAGGTGC
 AGTGGCTCAGCTTGTATTTCCAGCACTATGGGAGGCCAAGGTGGGTGAGCCACGAGGTCAA
 GAGATGAGGACCATCTGTGCCAACATGGTGAAACCTGTCTCTACTAAAAATCAAGAAATTA
 GCTGGGCGGTGATGGTGCAGCCTGTAGTCCAGCTACTTTGGGAGGTCGAGGCGAGGATTCG
 CTGGAACCGGGAGGTGGCAGTTGCACTGAGCTGAGATCGAGCCATGCACTCCAGCACTGGT
 GACAGAGCGGACATCCATCTCAAAAAAAGAAAAAAGAAAAAATGGAAAAACATCC
 TCAATGGCCACAAAATAAGGTCTAATTCATTAATATATAGTACATTAATGTAAATATAATATTA
 CATGCCACTAAAAAGAAATAGGTAGCTGTATATTTCTGGTATGAAAAACATATTAATAT
 GTTATAAACTATAGTTGGTGGCAAACTAATGTGGTTTTGGCCATGAAATGGGCATTGAA
 ATAAAAGTGAAGAAGATCTATACCAGATGTAGTAACAGTGGTTTTGGGCTGGGAGGTGGA
 TTACAGGAGCAATTTGATTTCTATGTTGTGATTTCTATAAGTTGTTGAATTTGTTTGAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSONLLQHKNDENCSPWETVVNMNLSYNKLS
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMAIRELNIAFNFLTDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCCTCELKNFIQLETYSEVMVGVWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCCCLHFDLPWYLRMLGQCTQTHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSI FVLSPNFVQNEWCHYEFYFAHNNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRCKGLEFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

[illegible]

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPIYYARPEPELETFSPLP
AGPGEEWERRPQEP RPPK RATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRNLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLDPDNYYHRRNEMTT
TDDLDFKHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG
SELGGWSLGRWTHDGDIDINNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAMMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTEHTPTPDDHVFRWLAYS YAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGI PNAAISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRKRRQRG

CTAAGAGGACAAGATGAGGCCCGGCTCTCATTCTCCCTAGCCCTTCTGTCTCTCTGGCCAGCTGCGAGGG
ATTTGGGGGATGTGGGACCTCCAAATCCCGCCCGGGCTTCAGCTCTTCCCGAGTGTGAATCACTCAGCTCGG
TTCAGCTCCAGCTCCAGGTGGGCTCAGCTCCAGCCGAGCTTAGGCAGAGAGTTCGTGTGCCAGTGTGT
TTCCAAATTTCCCGGCTCCGTGTAGTCACCTGGGACCTCCAGTGTCTCTGTTCCCTGCGAGACAACCTTTT
CCGTGCAGACAGTGGAAAGCTTGGAAATGACAGCTCATGTTCTTTCCAGAAATTTGAGAAAGAACTTTCAA
GTGAGGGAATATGTTCCAAATTAATAGTGTGATGAAAGAAAGCTGTAAACCTAACTGTCCGAATGACATCAT
GGAGAAGATACATTTTCTACAGTAACTGGACTTCAGCTGATGACAGTAGAAGTGAAGGAGATGGAAAAAG
TGTGTATACAGCTGAAGGAGAGTTTGTGGTGAAGCTCAGAAATTTGTGACGACCTGGAGTGTGGATTAAGAA
AGTACACTCTTGGTAGAAGACTTGAGACATGAGCAAAAAAATGTTCTTCGATTCCCGGAGAAATCTGTGC
TCTGAGACCAAGAGTGAAGAGTGTGAGGCTCTAAAGATCAAAACACCCCTGTGCTCCAACTCTCCCTCCATC
CAGGGAGTGTGGTCATGGTGGTGTGGTAACATGACCAACCTCTGTGGTTCAGCTCAACTGGAGAGGGTTT
TCTTATCTATATGGTGTCTGGGGTAGGGATTACTTCTCCCACTCAAAACAAGGACTTATTTGGTGGGCGGCC
ATTGAATACAGATGGAGACATTGTGAGTATTAAGTACTACACACACTGATGATTTGCTATGTATATA
ATGCTCCGAGATGCGCATCACTATGCCAAGTACGATGTGTACAGAGTTTACAAACAACACTGTACGTCAAC
ATTGACAAACCCGGGAATATGCCAGATTAACCTAGACCAACACAGTGTGCTGTGACTCAACTTCCCTAA
TGTCTGCCATATAATACCGCTTTTATATGTCTAATGCTTGTCTGGCAAGATATGACTTGTGTGGATGAGAAT
TGCTGTGGGTATTATTACAACTGAAGCCAGCTGTGTAACTGGTGATAGTAAGTCAATGACACCAACTT
CAGGTGCTAAACACTTGGTATACCAAGCATTAAGCAATCTGTGCTTCAAGCCCTTCATGGTATGTGGGGTGT
GTATGCCACCCTGACTATGAACACAGAACAGAGAAGATTTTACTATTGACACAAACAGGGAAGAGGG
CCTAACTAGACATGTGATGCTATGATGAGTGCAGAAAAGTGCAGAGACTTAATCTATAACCTTTTGACCAAGAA
CTTTATGTCTATAACGATGTACCTTCTGAATATGATTTCTGTCTGTGCAAGAACCCCTGAACTGCTTTA
GGAGTTAGGGTGAAGAGGAAAATGTTTGTGAAAAAATAGTCTTCCACTATTAGATATCTGCGAGGGGTGT
CTAAAGTGTGTTCATTTGTGCAAGATGTTTAGTGTCATAGTTCTACACACTAGAGATCTAGACAGATTGTCT
TGATTTGTGTGAGTCTCTTGGGAATCATCTCGCTTCTCAGCGGCATTTTGAATATGAGTCTGTGTAGGGTGGGA
TGTGACAGCTCTAGGGGCATCTGGGCTAGTGAGCCACTCTGTAGAGGCTCAACTGAGAAGCTTTAATAT
GGAATTAAGGAATTTAAACTCATGATGGGCTTAGGGATCTTGTATACAGAAATATTGCCCAATGACTAGTCT
CTCATCTCTAGTACACCACTAATTTCTCATGCTCGAAGAACTCGGGACCTAGTAGGTAGATTAATATCT
CGAGCTCTCGAGGGGACCAATCTCAAACTTTTTCCTCCCTCATGACACTGGAATGATGCTTTGTATGTGG
CAGCATAGTAAATTTGGCATGCTTATATATTTACATCTGTAAGTGTGAGTTTATGGAGAGAGCCCTTTAT
ATGCAATTAATTTGATACGTGCAAAATTAATCCCAAGAGGATCTGATAGTGAAGCACTGCTTTTCTTCTCT
ATTGTCCACTCTATAAAGTCAAGTGAATCTCTACCTCTAATCACTTCCCTCAAAGGCGACTGAGAAGATAG
AACCAGACTCTATACCAAAATTCACCCCCCAACCCCTCTCTACTGCCATTTAAAAAAATTAATAGTTTCT
CTATGACAGTATCTAAGATGAGAAAAATTAATTTCTTAATTTCAATATGGAATTTTATTAACGACTCTA
AGACTATAGAAAATCTGTATGGCAGTGACAAAGTGTAGCAATTTATGTCTATATTAAGACCTTTGGAGCAT
TGTGCAACTTTTAGTGATGTCAGTTGTGATGTAAATTTTGCCTTTGTTTAGCCTGGAAGCTGTAGAAAAT
GAAAATTTAATTTTTTTCAGACGAGCTATGAAAAGCTATTGAGAGATCTAGTTAATCTAGTCGAGTGTG
TGGAAACCTGTGGTGGTATGTGATGTGCTGTCTGTGTTGAATGACTTATCATCTAGTCTTTTGTCTATTT
TCCTTTGATGTTCAAGTCTAGTCTATAGAGTTGGCAGTTTAAAGCTTTACTCCCCCTTTAAAAATAATGAT
TAAATGTGCTTTGAAAAAATAAAAAAATAAAAAA

FIGURE 38

MRPGLSFLLALLFFLGQAAGDLGDVGPPIPSPGFSFPGVDSSSSSFSSSSSRGSSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCCQSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTFPVVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGlyWVAPLNTDGRLLLEYRlyNTLD
DLLLYINARELRITYGQGSgtAVYNNNMVYNMYNTGNiARVNLTNTIAVTQTLPNAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTeASTGNMViSKLNDTTLQVLNTWYTKQYKPSASNAF
MVCgVLYATrTMNTRTEEIfYyyDTNTGKEgKLDIVMHKMQEKVQSINYNPFdQKLYVYNDG
YLLNYDLSVLQKPQ

0002521-11401

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAGGNATGTATTGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

000001.11101

FIGURE 40

TCTCGCAGATAGTAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGTGGAGATGGGGAGCGCTCTGGGGCTGTGTCTCCATGGGGAGCT
 GGATACCACTTTTGTGGAAGTGCCCGTGTTGGCTATGCCAGTGCTGCTAGTGGAAAC
 AACTCCCACTTAACTAGATTGATCTAGCACTTTTCTGGCTGTTGGAGTATGTGTAGCTTG
 GTAATGTTGATACCAGGAATGGAAGAACAACTGAATTAAGATTCTGGATTCTGTGGAAGTG
 AGAAAGGCTGTGTCCTTGTAAACATTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTTTGGCTATGTTCTATCTTCTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCCTTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTA
 TTATTGGGCTATTCTTCTTCCAGAAGGAACTTTACAAGTGTGTGGTTTATGTAGGCCATG
 GCAGGTGCTTTTGTCTCATCTCATACAAGTCTTACTTATTGATTTTGCACATTCATG
 GAATGAATCTGGGTTGAAAAAATGGAAGAAGGGAAGTGCAGATGTTGGTATGCAGCCTTGT
 TATCAGCTCAGCTCTGAATTAATCTGCTGCTTTAGTTGCTATCGTCCTGTTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTCAGAAAAACAGGCTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTTCTGTAATGCTATATCTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTT
 TGTTACAGCTTCAGTAATACAGTCTACACAATGTATTTGACATGGTCAGTATGACCAAT
 GAACCGAAAAACAATTCGAACCAAGTCTACTAAGCATAATTTGGCTACAATACAACAGCAC
 TGTCCCAAAGGAAGGGCAGTCACTCAAGTGGTGGCATGCTCAAGGAATTTAGGACTAATTC
 CTCTTTTGTGTGTGTTATTTTATCCAGCATCCGTAAGTCTCAAACAATAGTCAGGTTTAATAAC
 CTGACTCTAAACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAGAATGATGGAAT
 ACTGGAGAGTGGGACGATGTTCAACCGAGTGTAGATTAATGAAGGGATGGTGTCACTTACA
 GTTATTTCTCTCTTTCACCTTCACTGCTTTTCTGGCTTCACTTTATATCATGATGCCCTTACC
 AACTGGTCCAGGATGAACCCCTCTCGTGAGATGAAAAGTCAGTGGACAGTGTCTGGGTGAA
 AATCTCTTCCAGTTGGATTGGCATCGTGTGTAATGTTTGGACACTCGTGGCACCCTTGTTC
 TTACAATTCGTGATTTTGACTGAGTGTGAGACTTCTAGCATGAAAGTCCCAGCTTTGATTATGTC
 TTATTGAAAAACAGTATTTCCCACTTTTGTAAAGTTGTGATGTTTGTCTTCCATGTAAC
 TTCTCAGTGTCTGGCATGAATTAGATTTTACCTGCTGTCATTTTGTATTTTCTTACCAA
 GTGCTGATGATGTGAAGTAGAATGAATTCAGAGGAAAGTTTATGAATATGGTGATGAGT
 TAGTAAGAGTGGCCATTTATTTGGGCTTATTTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACRAATTTGTTTGAATTTTAAAAATATATAGACCTTAAGCTGTTTGAAGCATTTAAA
 GCAATGATGGCTGCTTTTGAATATTTGATGTGTTGCCCTGGCAGGATCTGCAAGAAGAAC
 ATGCTTTATTTTAAATTTATAAACAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGCTTTTACCTTTGATACGGAATTTACACAGGTAGGGAGTGTGTTAGTGGACAATAGTGTAGG
 TTATGGATGGAGGTGTCGGTACTAAATGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGGCAACAAAGTGAAGCTGTTTGGTTGTTTTAAATCTATGAAGTATGGGTTCAAGT
 GGAATGTTTGAAGTCTGAAGGATTTAGACAAGGTTTTGAAAGGATAATCATGGGTTAGA
 AGGAAGTGTGTTGAAGTCACTTTGAAAGTGTGTTTGGGCCAGCAGGTAAGCTCACCCCT
 GGTATCTCCAGCACTTTGGGAGCTTAAAGTGGGTAGATTACTTGGCCAGGAATTCAGACCA
 GCTTTGGCACAATGGTGAACCTGTCTTATAAAAAATATCTGGCTTTGAGCATATGCTCTGGTCT
 CAGCAGCTGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGTTGAGTGGAGCAAGTCA
 CGTCACTGCACCTAGCTGGCAGAGTGAAGCCAAAAAATATATATATTTGAATCAAGG
 AGGCAAAATTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGCTACTAT
 ATAAAACTAGTCCAGTTCTCTCATTAAAAAATGAAGACATGAATACAGACTTAATAA
 CTTCAGATAGCTAATTAGGAATTTCAAGTTGGCCAATAATAGCATTTCTCTGACATTTAA
 AAATAATTTCTATTCAAATACATGCATATTGATTTACACCTCATACTGTGATAATTAATGT
 GATGTGGATTGATGTTGAGCATGACCATTAACAGGTGAGAGGAATGATGAAGATGCTTTT
 AGAATAAATCTGCTTATAGTATACACAGTTCAAAGATGTTTAAATGCTTTTGTAT
 TTACTGCCATGTAATTTGAATAATATAGATTATGTAACCTTTCACTGAAATCAAGCAGT
 ATGAGAGTTTGTGTTTGTATGTGCTAGTGTCTAATGAGCTTTTAAAACTCAACAT
 TCTTTCTTAAAAATTTTAAATGTGAATGGAATGAATTAACAAATTCAGCTTAATCCCCAAC
 TTATCTGTGTGTAGACATTGATTCCACAATTTGAATGGCTGTGTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

00000000-11401

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLRCCPCSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVPNCNILVGKYKAVYRLCFGLAMPYLLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAI IIGAFFIPEGFTFTVWFVVGMAGAFCFILQLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALSLATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSSLISIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFFYSSIRTSNNQVKNLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVYTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTA VVVKISSWIGI
VLYVWTLVAPLVLTNRDFD

GCAGGAAAGAAGCTGCTCCATCTTGTCTGTATCCCGCTGCTTCTTNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGAAACAANTCCACTGTAAC TAGATTGATCTA
TGCAC TTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTCTCTTAAATTTGCTGCAGCAATTGCAATTATTATTTGGGGC

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCGTGTTTGNATGCCGATGCTGTCCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACCTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGGAACAACCTCCACTGTAAGTAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACATTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT
ACAACTGTGTGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAC TAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGTTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTCAGAAAACAAGGC
GTTCA TCAGTGTC AACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

[illegible]

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFNAFVTPMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHES
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPEFDIRVPPFYVRGPNVEAGCLNPHIVLNIIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDAQ
PRNLTKRHWPAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDLKYKS
LQAWKDKHLIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRLLKRGSSL
HPRKGLQEAKDKVLLREQKRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNTYWCMTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGAAAA
CCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGCGGGGCCACCTGGGAATCTTTACC
ATCACCGTCATCTTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCACCAGCCACCATCCCCGCCA
CGCTCGCTGAAGGCTGCTGTGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGTCATGGCATGCCCAGTGTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAAGGGGAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTCATCGGTGCCTTAGTCCAAGAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRRAQWPWFR
RRGHLGIFHHHRHHPGHVSHVPNVGLHHHHHPRHTPHLLHHHHHPHRRHPRHAR

FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTA
CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
TGCAGCATCTCTCCAAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATCCTCGGCTGG
AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCCACTGGCACGGCAGGGAGACTTCTAT
GTGCCTGAGATGAAGGAGACAGAGTGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAAGCTTGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTGA
GGAGCTGGACTTGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAGTAACCC
ATGGCCTGCACCCCTCCTGCAGTGCAGTTGCTGAGGAAGTGAAGAGTCTCCAGCAGACTCT
CCAGCCCTCTTCTCCTTCTCTGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC
TCCAGGCCCTCTGCTAAGCCTTCTCCTCACTGCCCTTAGGCTCCCAGGGCCAGAGGAGCCA
GGGACTATTTTCTGCACAGCCCCCAGGGCTGCCGCCCTGTTGTGCTTTTTTTCAGACTC
ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTTCACCTGGAAAAAA
AAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCavgSILSEGEESpSPeLIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHfMCPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSaATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEgPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGT**CATG**ACCCCTGCGCCCCCTACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

090211 1410 1

MTLRPSLLPLHLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPECAEPAAFGDTLHI
HYTGS�VDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSPADAVVQYDVIELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

MTLRPSLLPLHLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPECAEPAAFGDTLHI
HYTGS�VDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSPADAVVQYDVIELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCGGGAACGTGTTCC TGGCTGCCGCACCCGAACAGCCTGTCTTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGAGAGCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGAGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGTTATAGAACTTGGCCAAAAGCAGGTATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAAC TACTGGCTAAAGCTGGTGAAGGGCATT TTGCCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAACCGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAATAATAAATTTAAAAAACTTAAAA

CTGCTGTCATCCGGGTGTCCTGGAGGCTGTGGCGTTTTGTTTTCTGGCTAAAAATCGGGGGA
TGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
ACCTGAAAAAAATGCTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGG
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTACAGGCTGGTGGAT
TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
GGTGATAGTTACAGTGAAGGTTGCTGGGTCAACAGGTGCTCGCATTGGCTTTTCGTTGG
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
CTAAAGAAAAGACATAGTATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATCTTT
TTTGGAGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
TTCCACAGCACAAACAGCCCTGCATGGGTTTGTTTGTTTTTTACTGCTCACTCCCAACCTT
TTGTAATGCCATTTCTFAAACTATTCTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACCTTGATTAACCT
ATAAAATGTTAGAGGAAACTTTCACATGAATAATTTTGTCAAATTTTATCATGGTATAATT
TGTAATAATAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTACTTTTTTAAATATTCCGTGG
TCAAATTTCTTCTCACTATAATTGGTATTTACTTTTACCAAAATCTGTGAACATGTAAT
GTAATGGCTTTTGGGGTCTCCCAAGGGGTGAGTGGACGTGTGGAAGAGAGAAGCAACCAT
GGTCCAGCCACAGGCTCCCTGTGTCCTTCCATGGGAAGGTCTTCGCTGTGCCTCTCAT
CCAAGGCGAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
CACATCCACCACG

57/330

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

090224.11404

FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCACCCTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTCTGGGTCAAACAGGTG
CTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATAAC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

GGACACCGGGTTCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGTGTACTATTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
TTTGGGGTCAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATT
CTGATTGNATTCATGCGGATTCTTCTGGAGGTATGTTGCTAAAGAAAAAGACATAGTAT
ACCTTGGAAATTCNTNTATTTTTCCGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

099351-11104

FIGURE 62

GGGAGGCTGTGNCCTTTTGTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCCGGGAACCATTCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

10992321 11401

FIGURE 63

CGACGCGGGCGT**ATG**TGGCTTCCGCTGGTGTGCTCCTGGCTGTGCTGCTGCTGGCCGCTCC
TCTGCAAAGTTTACTTGGGACTATCTCTGGCAGCTCCCGAATCCTTTCTCCGAAGATGTCT
AAACGGCCCCAGCGCCCTGGTAACGACAAGGAGGCCAGGAAGAAGTTCTCAAACAAGC
TTTTTTCAGCCAACTCAAGTGCCGGAGAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG
GCGTGGCTGCAGCTGCATTTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGGTGGCAACAACAT
ACCAAGGCGAGGGGCTGCTGTGCATACCTTTGGAAGAATGGCCTTGAATTTGACACAGGAAT
CCATTACATTTGGGCGTATGGAAGAGGGCAGCATTTGGCCGTTTATCTTGGACCAGATCACTG
AAGGCGAGCTGGACTGGGCTCCCTGTCTCTCTTTGACATCATGTTACTGGAAGGGGCC
AATGGCCGAAGGAGTACCCCATGTACAGTGGAGAGAAAGCTACATTACAGGCCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGTGGTATCCA
GTGGAGCCCTCATGCCATCCTGTTGAAATTCCTCCATTGCCCTGGTGTGAGCTCCTCGAC
AGGTGTGGCGCTGCTGACTCGTTTCTCTCATTCTTCAAGCATCCACCAGAGCCTGGCTGA
GGTCTGTGCAGCACTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA
CTTACGGTGTCAACCCCAACACAGTGCCTTTTCCATGCAAGCCCTGTGGTCAACCACTAC
ATGAAGAGGAGCTTTTATCCCCGAGGGGTTCCAGTGAATTCCTTCCACACCATCCCTGT
GATTACGGCGGCTGGGGGCTGTCTCACAAGGCCACTGTGCAGAGTGTGTGTGCTGAGCT
CAGCTGGGAAAGCTGTGGTGTGAGTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC
CCATCGTGTCTTCCAAAGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC
CGCTGCTGCGAGTGTGAAGCAGCAACTGGGGACGGTGGGGCCGGCTTAGGCGATGACCT
CTGTTTTCATCTGCTGCGAGGCACCAAGGAAGCACTGCATCTGCCCTCCACCACTACTAT
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGTACGTCTCCATGCCAGGGAAGA
GGCTCGGGAACACATCCCTCTTCTCTTCTCGCTTTCCCATCAGCCAAAGATCCGAGCTGGG
AGGACCGATTCCAGGCGGCTCCACCATGATCATGCTCATACCCACTGCTACGAGTGGTTT
GAGGAGTGCAGCGGAGCTGAAGGGAAAGCGGGGCACTGACTATGAGACCTTCAAAAACCTC
CTTGTGGAGCCTCTATCTCAGTGGTCTGAAACTGTTCCCACTGGAGGGGAAGGCTG
AGATGTGACTGCAAGTATCCCACTCACCACCAAGTCTTATCTGTGCTGCTCCCCGAGGTGCC
TGCTACGGGCTGACCATGACCTGGGGCGCTGCACCTTGTGTGATGGCTCCTTGAAGGC
CGAGAGCCCCATCCCCAACCCTATCTGACAGGCGAGGATATCTTCACTGTGGAGTGGTGC
GGCCCTGCCAAGGTGCCCTGCTGTGCAGCAGCGCCATCCTGAAGCGGAACTTGTACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAAGAAAGAAAT**TAGT**TCCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCCTTGACAGTATAAGCACTCTAATTTGGTTCTGATGCCTGAAGAGAGGCCTAG
TTTAAATCACAATTCGGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTAGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG
TCTCATGACGAGCGGCGCTCTGCATCCCTCACCATGCTCTCCTAAGTCACTGATCAAAGCGA
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGAGCTCAACCTGGTGGGTTGAGTGT
TGCTCTGAGGCTTGTCTCTCATTTAGTGTACGCTGCACAGTCTACACTCTCAAGG
GAAAGGGGACACTAATGAGGCTTAACTCAAACCTGGGCGTGGTTTGGTGGCCATTCCATA
GGTTTGGAGCTCTAGATCTCTTTTGTGCTGGGTTCAGTGGCTCTTCAGGGGACAGGAAT
GCCTGTGCTGTGGCAGTGTGGTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGTGTGATCAGATGATCATATCCAATTATATGGAAGTCCGGCTCTGTCTTCTTATCA
TCGGGTTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACTGAGCCTCAATCAAGC
CTTATCCACAAATACAGAGGAGGTGTGGGTTAAGGAGGGAAGTGCATCAGGATCAGGGCA
TGGAGCTGGTAAGATGAATCTTGTGGGCTGAAGCAGGCTCGAGGGCATTCCAGCCAGGG
CAGCAGAGGGACAGTGTGAGGAGGTGTGGGTTAAGGAGGGAAGTGCATCAGAAAGGGA
AAGCCAGGGAATGTGTGTGAAGCCGAAATGGCAATTTGAGTTAATAGCACATGTGAGG
TTAGACAGGTAGTGAATCAAGCTCAAGGTTTGGAAAAATGACTTTTCAAGTTATGCTTTG
GTATCAGACATACGAAAGGTCTCTTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATTG
ATTCCATTGCTTTAAAAAATAAAAAA

FIGURE 64

MWLPLVLLLLAVLLLLAVLCKVYLGLFSGSSPNPFSSEVDKRPAPLVT DKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYYDTMDQAMERYVSMPREAAEH
IPLFFAFPSAKDPTWEDRFPRSTMIIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTGCLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

FIGURE 65

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTTGGCACCGGCCCCGAGAGGAGG**ATG**CGGGTCCGGATAGGGCTGACGCTGCTGCTGTG
 TGGGTGCTGCTGAGCTTGGCCTCGGCTCCTCGGATGAAGAAGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGACGGCAGA
 GTAGTTGCTGGTCAAAATATTTCTTGATTCAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAAGTGTACAGAAGATATCAGCTTTCTAG
 AGTCTCCAAATCCAGAAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAACCAGCTTTG
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTTCTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCTAAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTGGTGATTACTTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTTGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC
 TCTTGGCTTTCTGTATGCCTCTGGACTTGGTGTTAATCAAGTCAGGCAAAGGCTCTTGAT
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACTTT
 TCAGCTTTCATGATCCAGATTTGCTTGATTAAGACCAAATATTCAGTTGAACCTCCTTCAA
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACA
 ATTTTCTTTAAATGATTAGTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC
 TCTTTTTAAATTTCTCTGAGTTGGAATTGTCAGAATCATTTTTTACATTAGATTATCATAA
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAATGGTGGCTATAGAAAAACAACAT
 GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT
 GTGCAGAATGACTCCAGAGAGCTCTACTTTCTGTTTTTACTTTTCATGATTGGCTGTCTTC
 CCATTTATCTGGTCATTATTGCTAGTGACACTGTGCCTGCTCCAGTAGTCTCATTTTCC
 CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACTCATTTTTAATAAA
 ATTATGTCTAAGATTAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

CGCGGCTTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA

FIGURE 66

MRVRIGLTLTLLCAVLLSLASASSDEEGSQDESLSKTTTLTSDSVKDHTTAGRVVAGQIFLD
SEESELESSIQEEDSLKSQGEVSVTEDISFLESPNPENKDYEEPKKVRKPALEGTAGH
EPCHFPFLFLDKYEDECTSDGREDELRLWCATTYDYKADKEWGFCEEEEEAKRRQMGEAEMM
YQTGMKILGNSNKKSKREARYLKLQASMNHTKALERVSYALLFGDYLPNQIQAAREMFEK
LTGEEKSPKGTALGFLYASGLGVNSSOAKALVYTFGALGGNLIAHMVLVLSRL

FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGCTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAAATGCCT
GTGTCTCACCATTAGTCCCGTGACGCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

67/330
FIGURE 67

68/330

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVLAQLSCTLSPOHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFSP

0902521 111101

FIGURE 69

CGCGCCCGCCCGAGACCGGGCCCGGGGCGCGGGCGGGATGCGGCGCCCGGGGCGG
CGATACCGCGGAGCGACCGCCGCGGCGCCGCTGACCCCGCCGCGCCGCGCTGAGCCC
CCCGCCGAGGCTCCGAGAGCGCCGAGATGACGCGCGAGCCCTGTGTGCTCTGCTGCTCGG
CGCTGCTCTGTGGGCGCTTCCACCGCGCGCGCGCGCGGAGGCGCCCAAAAGATGGCGGAC
AAGGTGCTTCCCGCAGGTCAGGTCGGCGGCTGGGCGGCTGTGCGGCTGCAGTCCGCAATGGA
GGGGGACCGCCGCGCGCTGACCATTGTGGACCAAGGATGCGCCACCATCCACAGCGGCTTGA
CGCGCTTCCCGCTGCTGCGCAGGGGCTGAAGTGAAGCAGGTGGAGGGGAGATGCCGCG
GTGTACGTGTGCAAGGCGACCAACGGCTTGGGAGCGCTGAGCGTCAACTACACCTCGTCTGT
GCTGATGACATTAGCCCAAGGAAGGAGGCTGGGGCGCCGACAGCTCCTCTGGGGGTCAAG
AGGACCCCGCAGCGCAGCTGGGCGAGCGCGCTTACACAGCGCTCCAAGATGAGGCGC
CGGCTGATCGCAGCGCCCTGGGTAGCTCCGTGCGGCTCAAGTGCCTGGGCGCGGCGACCC
TCGCGCGGACATCAGCTGGATGAAGGACGACCAGGCCTTGACGCGCCAGAGGCGCGTGGC
CCAGGAAGAAGAGTGGACACTGAGCCTGAAGAACCTGCGGCGGAGGACCGGCAAAATAC
ACCTGCCGCGTGTGCAACCGCGCGGCGGCCATTCAACGCCACCTACAAGGTGGATGTGATCCA
CGCGACCCGTTCCAAGCCGTGCTCACAGGCAAGCACCCTGAACACAGCGGTGGACTTCG
GGGGACACCGTCTTCCAGTGAAGGTGCGCAGCGAGCTGAAGCCGCTGATCCAGTGGCTG
AAGCCGCTGGATACGGCGCCGAGGGCGCCACAACTCCACCATCGATGTGGGCGCGCAGAA
GTTTGTGGTGTGTCGCCACGGGTGACGTGTGCTGCGGCGCCGAGCGCTCCTACCTCAATAAGC
TGCTCATACCGCTGCGCGCAGGAACGATGCGGCGATGATCATCTGCTTGGGCGCAACAC
ATGGCTACAGCTTCCGACGCGCTTCTTCCACCGTGTGCGCAGACCAAAACCGCAGGGCC
ACCTGTGGCTCTCTGCTTCCGCGACTAGCCTGCGCTGGCGCTGGTGTATCGGCTCCAG
CCGCGCGTGTCTTATCTTCCGCGACCGTGTCTTGTGCTTTGCGAGGCGCAGAAGAACGCG
TGCACCCCGCGCTGCGCTTCCCTGCTGGGACCGCGCGCGGGGAGCGCGCGCACCG
CAGCGGAGACAAGGACCTTCCCTCGTTGGCGCGCTTACGCGTGGCGCTGGGTGTGGGGTGT
GTGGAGCATGGGTCTCCGGCAGCCCCAGCACTTCTGGGCGCGGCGCGCTGGTGTGGC
CCTAAGTTGTACCCCAAACTCTACACAGACATCCACACACACACACACACTCTCACAC
ACACTCACAGTGGAGGGCAAGGTCCACGACATCCACTACAGTGTAGACGGGACCGGT
ATCTCCAGTGGGCGCGGGGGCGCGCCAGACAGCGAGCTGGGAGGATGGAGGACGGAGCT
GCAGACGAAGGCGAGGGGACCATGGCGAGGAGGAATGGCCAGCACCCGAGCGAGTGTGTGT
TGAGGCATAGCCCTGGACACACACACACAGACACACACTACCTGGATGCATGTATGCAC
ACACATGCGCGCACACGTGCTCCTGAAAGGCACACGTACGCACACGACATGCACAGATATG
CCGCTTGGGCACACAGATAAGCTGCCAAATGCACGCACACGACAGACATGCCAGAACA
TACAAGGACATGCTGCTGAACATACACACGACACCCATGCGCAGATGTGCTGCGCTGGACA
CACACACACACACGATATGCTGTCTGGACGCACACAGTGCAGATATGGTATCCGGACACA
CACGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCTTGACACACACATGCACGG
ATATTGCTTGGACACACACACACACACGCGTGCACAGATATGCTGTCTGGACACGCACAC
ACATGCAGATATGCTGCTTGGACACACACTTCCAGACACACGTGCACAGGCGCAGATATGCT
GCCTGGACACACGAGATATGCTGTCTAGTACACACACACGACAGATGCTGTCCGGACAC
ACACAGCATGCACAGATATGCTGTCCGACACACACACGACGACAGATATGCTGCTGGAC
ATGCACACAGATAATGCTGCTCAACACTCACACAGTGCAGATATGCTTGGACACACACA
TGTCACAGATATGCTGTCTGGACATGCACACAGTGCAGATATGCTGTCCGGATACACAGC
CAGCGACACATGCAGATATGCTGCTGGGACACACTTCCGGACACACATGCACACACAGGT
GCAGATATGCTGCTGGACACACACACAGATAATGCTGCTCAACACTCACACAGTGCAGAT
TATTGCTTGGACACACATGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATAT
TGCTGTCCGGATACACACGACGCACACATGCAGATATGCTGCTGGGACACACTTCCGGA
CAGCATGCACACACAGGTGCAGATATGCTGCTGGACACACGACAGCTGACGTGCTTTGG
GAGGTGTGCGGTGAAGCTGCAGTACGTGTGCGGTGAGGCTCATAGTTGATGAGGACATTT
CCCTGCTCCACGCTCACTCCCCAACTCTGCCCGCTCTGTCCCCGCTCAGTCCCCGCTC
CATCCCCGCTCTGTCCCTGGCCTTGGCGGCTATTTTTGCAACTGCTTGGGTGCCGAG
AGTCCCCCTACTGCTGTGGGCTGGGGTTGGGGCGACAGCGCCCCAGCGCTGAGAGGCTGGAG
CCCATGGGTAGTGGCTCATCCCGAGTGCATTCCTCCCTGACACAGGAAGGGGCTTGTA
TTTTATTTTAAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTGCGAGGAC
GTGTGCTCTCTCTGGGGCGCGGACCGCGCTGCTTACGACCTGCTGATGACCAACCCCG
GTCAGGCGACAGCAACCCCGACCCCACTGTGCTGGTGGCGCCAGATCTCTGTAAATTTTA
GTAGAGTTTGAGCTGAAGCCCGGTATATTTAATTTATTTGTTAAACACAAA

09992521.11401

FIGURE 70

MTPSPLLLLLLPPLLGAFFPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFTVLVLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSAAAPQHLLGPGFVAGFKLYPKLYTDIHTHTHTSHSHVEGKV
HQHIHYQC

FIGURE 71

CCGAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAATCTCCGAGGGGACCGCATTCCAGAGTC
 AGTCACTCTGTGAAGCACCCACATCTACTCTTGCCACAGTCTCCACCGGGCTTGGGGGAAAGATGCTGGGGAGGACA
 AGGGCTGGGTGTTCTCTCTCTGGTCTCTGGAAGTCACATCTGTGTGGGGAGACAGACATGCTCAACCGTCA
 TGAAGAAGAGTCCAGCCTGGGAAGAGAAACCCAGCATCTTTGCGAAGCCTGCCACACCTGGAGAGCCTGG
 TGAGTGGACCAACATGGTTCAACATCGACTACCGAGCGGGAAGGCGATTTGAGCGCCTGGAGCCTATTCCT
 TCTACTATGGGACCGCTGTATGTGGCCTCCCTGGGGCTAGAGGCTCGGACACTGATGGACACCTGGGGGC
 AGCATGGCCAGGTGGTCCATGGTATGCCCTGGGAGGTTTCTGGTGCCTCAACAGGGGACGAGCGGCTGGGCA
 GAACTCGCTTAATTACACCGATGAGCTCTCTCTGCCACAGGATGCTGCCGCGAGACAGAGGCGCATCTGGA
 GCCATGGTCTCCCTGGAGCAAGTCTCAGCTCAGCTGCGTGTGGTCACTGGGGTCCAGACTCCGACACGCAATTGCT
 TTGGCAGAGATGGTGTCTGCTGTGAGTGCAGGCCAGGCAAGAGGGTCACTGCACTGGGCGAGGACTACAGC
 CTGTGACCTGAGCTGCCCAATGGGCGAGGTGAATGCTCAGCTGTATGCTCATCTGCCAGAGTCTCATGCTC
 ATGGGGCTGTGCTCTCCGAGGAGTCCGCGAGCTCAGGGCTGCTATCTACTCTCTGACCAAGACGCGGAAG
 CTGCTGACCACAGACAGTGAATGGGAGATTCGGAATCCCTGGCTGTGCGCTTATGGCAAAAGCATCTCGAA
 GATCACAAGGTTCAAGTTTGCCCCATTTGATCTCACAATGCCAGACTAGCTGAAGGAGCGCCACCATCAAGG
 CAGATTTTGTGAGGCGCAGAGACTCCATACATGGTGATGAACCTTGAGACAAAGACAGGAGAGCTGGGCAGAG
 GTGCTCTGTGCTGTAAGGCGCAGAGGAGGCCAGGCCAGACAAATATTTTGGTATCATATGACACATTTGCT
 GGATCCTTCCCTTACAGACATGAGAGCAAGCTGGTGACAGGAATTCGACAGCAAGCCTGTAACTGATGCTG
 TTTGCAAGGCCAGAGTCATGCTGGGCTGTGAATCTCAAGATTCGACAGCTGATTTGCACAGCATCTGATGAG
 ACTCCTTGCAACAGGACTCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTCGAATGAGCCCAACT
 CTCTACTATGACGCTGGGAGGCTGCCCTGTTAAGACTTTGTGAGGGCAGCAGGATATGGATGCCGCGTG
 ATGCTGTGCAAGACTGCTGTGGCATCTCCAAGCAGAGGAAGGAGATCCAGTGCAGTGGCTTACAGCTACCC
 ACCAAGGTGGCCAAAGGTGACAGCTGCCAGCGGTGTACGGAAATCCGAGCATCTGCCGGGCGCTGTGCTGCT
 TGCTGCAATGGGGAGCCCATGCCCTTTGGCATGTGTACATGGGAAGCAGCCTGTAACTGATGCTGCTTACA
 AGGCACTTTCACTCTCATGTTCCCGAGGACACTGAAGAGCTGGTCTCACATTTTGGGACAGGCTGCAGAG
 TTTGTCAACACCAAGAGTGTACTTTCAACAAGAGGGGAGTGCCTGTGTTCCATGAATCAAGTGTCTTTCG
 TCGGAAGAGCCCATCACTTTGGAGCCATGGAGACCAACATATCCCTCGGGGGAATGGTTTGGTGAAGAAC
 CCATGGCTGAATCGAGAGATTCATCCAGGAGTTTCTACAGGCAGATGGGGAAGCTTACATAGGAAGGTGAAG
 GCGGCTGTGACCTTCTGGATCCCGGGAATATTTCCACAGGCCAGCTGCCAGACTGACCTGAATCATACA
 TGCGAGGAGGACATCTTCCCTTTCGACCTATGSCATGTTCTGTGGAATCTCAGAGTGAAGCTCACTTCAG
 AGCCACTTAATGCTGCAGAACTGAAGTCCACCTGACTCGACCCAGGTCAAGATGCCAGAGCACATATCCACA
 GTGAAACTCTGTCTACTCACTACAGACACAGGGCTGTGGGAGGAGGAAGTGATTTCAATTTGAAATCAAG
 GAGGAACAAAAGAGAGACAGAACTCTCTGGTGGCAACCTCGAGATTGCTGAGGAGGAGCTCTTTAACTGG
 ATGTTCTGGAAGAGCGCGGTGCTTTGTTAAGTGTAGGGGCTACCGGAGTGAGAGGTCTTTGCTGCTAGTGAGC
 ATCCAGGGGTTGTGATCTCCGATTAACCTGAGGCTGAGGCTAGAACTGGCTCTGTTCGAACCTCAGGGCTGGG
 CGGCTTTGCGAGTGTCTACACAGGCCACCGAGCGGCTGTGGCTGCCCTTCTGTATGAGCAAGTCCCTGATG
 CCTACTCTGCTATGCTTTGGCAAGCTGGTGGGAGGAAGCTCGAAGCGTGAGGTCTCTCTCAATTTCAAC
 CCAATGCAATTTGGGCTCCCTCAGCCCTATCTCAACAAGCTCAACTACCTCGGAGCGACATGAGGATCAAG
 GGTAAAAAGACAGCTTCCAGATTAGCATGGCCAAAGCCAAAGGCCAACTCAGCTGAGGAGAGCAATGGGCCA
 TCTATGCTCTTTGAGAACCTCCGGGCAATGTGAAGAGGCCACCCAGTGCAGGACTCTCCGGTTTCCAGGAT
 GAGGGGGATCGATATGACTACACACAGTCCCTTCAAGAGAGTGAAGCTCTGAGGCTGAGTGAAGTACTAT
 GCAATGTGCGCAAGCTATGGAATTCAGGCTCTGCTATCAAGTGAAGATTTTGGGGCCAGTGGAAGTGA
 ATGTGCAATCCGCAACATGGGGGCACTCATCGGCGGACAGTGGGGAAGCTGTATGGAATCCGAGTGTGAGG
 AGCATCTGGGACAGGAGCCAGCCCAATGTCTCAGCTGCTGTCTGGGAGTCAAGTGCAGTGGGATGCTCTATGA
 TCAGGACCGTGTGGACCGCACCTGGTGAAGTCTATCCCGGAGGAGTGGCCCTGAGGCACTGTGAACCCCA
 TGCTGCATGAGTACTGGTCAACCACTTGCCACTTCAGCTCAACAAGCAGCAGCTGAGTACACATGCTGGCA
 CCTTTGACCACTGGGCGCACATGTGAGCTCTGAGCTCACTGACAGAGCACTGACAGGCTCCAGGCGCAAGGAT
 CGGCTCGGCGCTTTGATGGACATCCGATGCTCTCCAGAATCATGAAGAGTGTGGGATGAGCC
 TCACCTTCACTCTGTAGAGAGGCACTAGGCGCGGAGGCTCCGATCTCCAGACTCCCAAGGACCCCGAGCCAG
 TCCCTCTCGAGGCACTGTCCAAAGGAAGTGCCTCGAGGAGGCAAGCAGGAGCGAGCGAGGCTGGCCAGGC
 CCAGGTTGGAGTGTGGCCTCTCTGAGATTTCTAGAGTTGCTCAACAGCGCCTGATCAACTAAGTTTGTGGT
 ACTTACCCCTCTTCTGGCCCTCATTTCAAGTGACAGCATTGTGAGCTGATGCACAAATGCACTGCTTAAT
 TGAAGCACTTCTCTTCTGCTATGCTTTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT
 TTGGCAGTGGGCCCCCAATGGCACAATAAGCCCTTTGTGAATCTGTTCTTTAATGAACACAGCAAAAT
 TGCCACTGGTAAAACTCTGAGCTCTCAACTGTACTTCAATTAATGCCATTAATGCAATTACTTCTCTCTT
 TTTTGCACTGGTTTGGCCCACTTCGCAATAGTGAATCTGATGCTGAGATCAATTAACCAATATAAGCATAT
 TCTTGTGCGCTTGTCTCCAGGACATAGGCAAGCTGTGATCATAGTTCATACATATAAGTGGTGAATTAAT
 AATAAARACACATATCTTACTTGAATGTAAATACATTAATTTCTTGTAAATTTGAAATCTGATGCT
 ACATCAAACTGAAGTAAATATATGAGGACATCAATCTCTTCCAGGCTGGAAGAGCACTCTCCAGG
 ATCAACATCAACAGGTGTCTAAGCTGATTTGTACATTTCCCTTCCGTTTCTTGTCTGCTGATGAGT
 CCAGTGTAGCCGAGGCGAGTGTCAATAATGATACTCTGATTTGCAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPISIFAKPADTLESPGEWTTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLLEARTTDTWTAGSTGQVVHGSPPREGFWCLNREQ
 RFGQNCNSYTVRFLCPPGSLRRDTERIWSPPWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLTTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAIYLLTK
 TPKLLTQTDSDGRFRIPLGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQNATNSFYDVGRCPV
 KTCAGQQDNGIRCRDAVQNCCGISKTEEREIQCSGYTLPTKVAKECSCQRCCTETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTfVDRLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
 KASVTFLDPRNISTATAAQTDLNFINDEGDTFFPLRTYGMFSVDFRDEVTSEPLNAGKVKVLH
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVYRYSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRRTDHEDPR
 VKKTAFAQISMakPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPVFN
 EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLVKVIPQGSRRASVNPMLHEYLVNHLPLAV
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
 FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGQRQGGVVASLRFPRVA
 QQPLIN

TCGAAGTTTGTAAAGCGCTAACACAAGATGTTAGGCTTCACCAAAAGCTCCTAAATATACCTGAATACAGAC
 AATCTTCTAACTCTCATATTGTTGGTATGCTCTTGAGGCTCCATTCATTATAAAAAAACATACGAG
 ACCCTACCTACCGCTACGCATACATATGTTGTATATATTGTAACATAGACAAGATCGCATCAATAAGC
 AAGCTCTGCTTTAGTTTCCACAAGATTACAAGAAATTAGAGAAGTATTCTCAGAGTCTGTCGATTCTATG
 CCTTTGGGTTACGGTGTCTCAGTGATGCAGCGCTATGGTTTGGTTGGGACATTATGATTGTGTAAAGCT
 CAGATTTCACGGAAGAGGGAAGAAATTTGGGATATCATGGGCTCGACGCGGACATACAGGCATGACAAATA
 TCTGAAAGTGAAACTCGATCTCGGATATTACCTGTGGAGACCTCTCGAGAGCTTCTGTGCAATGGGCAAT
 CCGTACATGTGCAATATGAGTGTATGCGAGCATACCTCTGAGTCGAGACACCCCTGAGCTGATGTGTTGATT
 GAGAGAGACATCCCTCCAAATTTGGGAGTCTGCCATTTGGAGGGAGTATCCGAGCCTCTCCAGGTTAACT
 CACTCTGCTTGGAGGCAAAACCTTAGTGATGCACACACATAGTTATTACTTTGAATCTGGGGCGCCGACG
 AATAGTCTCTGGAGAGCTCTCGATTATGACGACACATGCGACGCTCATGATTATGCACAGAGCTGCTTGA
 AGTCTTCTTACATGTGATCTAAATCCGTGAGGATATATACAGCATACGSGTCTAGGAATCATTTGCACAGA
 AGAGTATCAACAGAGGTATACAAACAGGTACAAATATCCACTTTGAAATCAAGAAGAGGTTGCGCTTTTGT
 CTGGAGCTCGGCTACGCAATATGGCTTCCTCTACGCGACAGTCTGACAGCAAGAAGATACAGAGATTCTTGT
 ACAGTCACAGACCTGAGGATAAGGCTTTAGACCGAGCGTTGGGGAATATTGTAGATGAGCTACACTTGGC
 AGCTGATTTTACGGAGCTTCAGACATAAAGGTGGCAGGAGAGGTGCAAGTGTATTCTCCATGCCACTTATGTG
 TGTTGACAAACGCAAAATGACATCGGAATGTGAGCACAGCACTACAGTGCAGATCTGGGAATACGCAAG
 AATTTATCAGGCGGACCTGGAGTCGAGCTGCTTATCTCCCTCCCAAAGGCACTGCAAAATCGCTGATCC
 CAGTTATTCAGTAAATTGGTACGAATGTCTGCGACAAGCAGAGCTCTGCGATCGCAAGCGAGGAGTGCGACA
 CAACAGTGGCTGCTGCTGTGCCGGCGCATACACAGGGCATCTCTCGGAGAGAGTGCGGTGGAGAGAGGCTGCG
 AGCTCGCGCTCGCATCTGGCCAGGGGGCGCCCCGACGCGACCGCAGCTGCTGCTGTGACCGAGCTGCTG
 GACACCGCCGACGCCCCCTGGTGTCTTAGTGTCACTCTCAGCCACACCGGAGGGGCTGTGCGGTGGGGAGCA
 GGGCAACCCCAAACTTTGCTATCACTTAGGAAACATACAGACACAGCCCCATCAGACGTGACGTACAA
 CTAAAGAGGCGCTAACTGACATTAAGCATATTTATCACCCTGGGACAGCATCTCGAGTACAGCATGTTAATTTG
 TGACTCTCAGAGGAGTTGGCACTGTGTATATTATCACTGCAAAATCACTTGCAGCTCGAGAGTATTTGGA
 TTGGAAGAGCTCGGACAGCCCCCAACAGGAAAGCAAAAAACAACAATCAACCGACTAAAAACATTTGGC
 TACTCTACGCTGGTGGCGCTTAGTACGACTCGCGCAGTGTGGGACACCAAAATAGCATTTCTGCTGCTGAC
 GTGCTATTGTGGGATACAAAGGAATCTGTACAAGCTGCCATTGTGGCTCTCGCTCGCTCGATCCCTTCCAC
 TGTGCTTTTGTGTAAGCTTGCTCTGTAAACCTGTTGGTTGAAGATTCTTTGTCTGATGTAGTATGATGACA
 TGTGTACAGCCGCCCCCTCTAAAGCGCCAGGCACTACACCTCGTATATCTTACGACAGCATGAGTCGAGTGGC
 GCACACCCCACTACAGAAGTGGCTATAGGAAAGAAGGATGTACTCTCTTTGATTCAATGAGTIT
 ATTTTCTTGAATCTGTAATGTAGATTTTTGTATTATTGCCAATTTGTGTACCGACATCTGTTAAT
 GTATCTAATTGACATCAGCAAGATGTGACATTTTGTGCTCTCTTGGTCTTTGTTTCTGTGCTGCGACA
 GATTTCTCTGTAGGCGCAGGAGCTGTCTGGCATCAAGAATATCATGTTACATATACAAGTGTAAATAGA
 TTTCCACAAAGGACATCTCAAGTGTCTTGTGCTTTAACTCGGAGATTAAAGATATAAAATCTCTGCA
 TAAAGCGTTTCAGGAATTTGTTATGCAATTTCTAGAGTGAAGGACAGGCCACCAAGCATTTTCACTACTCT
 TTAAGTATTTCTGTGTGGACTGAGTACATCAGTGCAGAAATTAGTTCGAGGAAGATGGATTGATGTTCACT
 AGCTTGGACAACTTCTGCAAAATATGAGTATTTCCACTTGGGAAAAATTACACAGCAAAAAAAAAA
 AAAAAA

MYLSRSLSIHALWTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQLHTVLEIICTEESTGYTTSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFVTDLRIRLLRPVAGEIFVDELHLARYFYAIDIKVRGRCKCNLHATVCVYDN
SKLTCEHEHNTGPGDCGCKKNYQGRPWSPGSYLPIPKGTANTCIPSISSIGTNVCDNELH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQAPPHGTPALLLLTTLGTAS
PLVF

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCCGGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCTCTCATGACTT
 CTCTTGTGGACCATGTCGGTGATCTTTTTTGCCTGCGTGGTACGGGTAAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAAGATTTTTTGAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTGGAGACCCTGTGGTGGGAATTACAGCTTCTCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTGAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTACACACCGATGCACCTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTTCGAGGAGTTACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGACCAAAACCTCTGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAATCTTGCTGCTGGGGAATCTCATCAGCAGGAGCCTGTGGA
 AAAGGGCATGTCAAGTAAATCTGGGAATGGCTGGATTTCGGAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTTGCCACAAAGCGCCTTTTATTTAGGGTAAAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCTTACATTTATATGATTCTGGGGTT
 GCTTCAGAAAGTGTATTTTATGAATCATTATGATTTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTAGTCAGGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGAAGTAAATGGGTACATTTTAAACAACTCAGTAGTACAACC
 TAACTTGTATAAAGTGTGTAAAAATGTATAGCCATTTATATCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGTCAGAAATAATCTAAAGTGTATTATAAAAA

090527 11104
 10111 125260

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKVK
HFNYVSSSQMECSLEKIQEELKLPAPVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKVK
HFNYVSSSQMECSLEKIQEELKLPAPVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

TGCTTCTCTGGAGACCCFTGTGGTGGGAATTACAGCTTCNTATGACACTACCTGCATTGGCNT
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT
 TTAACATATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTGAGGAGGAGCTCAAG
 TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAAATGGGGT

CTACAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAACCGTGAGCGCGA
CCCCGACCTTAAAGAGCTGGGGAGCAAAAGGAGGACAGAGCCCTTTAAACAGCAGCGGGGTGGT
CTCGCCCTCTTAAAGGCGGGGCGTCGGAGCACTGTATCTGAGCCCCAGACTGCCCCAGTT
TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGCGCGCTT
CCTCCCCGCTCGCTCTCCCCGGGCGCAGGCGACTCGGGCTCAGTCATGCTGAGCAGCT**A**
TGGAAGCACTGTACTAGAAGTGCTATCGTGGAGAACAGCTATTCCAGAGGAGGATCCG
GAGTGATTATATCAACACTTCTGTTTGCACACACTGTACATCTCTGCCACATCTTCTTGA
CCGGCTTCAAGAAGCGCTGCTAGGTTACCACAGCTGGATGATGAAGATGCCACCGTCAACAAGA
TTGGCTGCGAGCTGTGACCTTTACCTTGCAATTGCGCTGGGTGCTGTCTGCTCTGCGC
TTCTCCATCATCAGCAATGAGGTGCTGCTCTCTCTCGCTCGGAACACTACATCAGTGGCT
CAACGGCTCCCTCATCTCATGCGCTCTGGAACTTGTTTTCTTCTTCCCCAACTGTCCTCA
TCTTCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
GGTGPTCTGGGCGGGTCTATGAGACAGCTGGTGATGTTGATCGCTCTCATCTGCTGGTGCT
AGGATAGTGTGGGTGGCATCAGCAATTGGAGCAAGAACAGGCCAACAGAGATGCACTCT
ATGACTTTTGGGAGTACTATCTCCCTACCTCTCATCATGCTCTCTCTTCTGGGGTCTGTG
CTGCTCTGGGTGTGATCTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
AGTCAAGCGCCCGCTGCTGGAAGACTGGAGGACAGCTGTAAGTCTCAGCCTTTGAGGAGG
CAGCCGCTGACCAGCAGGATCTGTAATCTACTTCTCTGCTGCTGCTTTCAGATCGAGCTGCT
TTACACAGACAGGTCCTGGCTCTGCAGACACAGGGCTGGTGTGGAGAAGAGGCCGAAGGC
TTCAGCCTGGCAACGGAACCTGGGCTACCCCTAGGGCTATGCTGTGCTTTGCTGGTGCTGACG
GCCGTGCTGTGCTCATTTGTGGCCATCCACATCTCGGAGCTGTCTCATGATGAGGCTGCCAT
CCCCGAGGATCAGGGGTACTCCTTAGCCAGCTCTCTCTTCCAAGCTGGGCTCCTTTGG
TGCCGTCACTCAGGTTGTACTCACTTTTACTAATGTGTCTCTCATGTTGGGGCTTCTATA
GCTCTCCACTCTTCCGAGCCTCGGGCCAGATGGCAGCAGCTGCCATGACCGAGATAATT
GGGAATCTGTGCTGTCTCTGTGCTCTAAGCTCAGCACTTCCTGTCTPTCTCGAACCCTGGG
GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGAGCCTTCAACTGGCTGGGCAATTTCTATA
TTGTGTTCTCTACACGCAAGCTTTGACGCTCTCACCACACTCTGTCTGTGTGAAGCACTTC
ACTCGACCTGTGCGGGCAGAGCTGATCCGGGCCCTTGGGCTGGACAGACTGCCGTGCCCGT
CTCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACAG**TGA**AGCTCCAGCTGGGGGTGGGA
AGGAAAAAATCGGACACTGCCATCTGCTGCTAGGCTGGAGGAAGGCCAAGGCTACTTGG
ACCTCAGGACCTGGAATCTGAGAGGTTGGTGGCAGAGGGGAGCAGGCCATCTGCATATT
GCATAATCTGAGGCAGAGTTTGGGACAGGACCTCTGCTTTCCATACTTAATCTGTGCT
CAGCATGGGTGAGGCTGGGTGACTGGGTAGCCCTGATGCCAAATCTGTTTACATCA
ATCTGCTCACTGCTGTTCTGGGCTACTCCCCATGCGCATGTTTACATGATTATGATGCAAT
AGGGTGGGTAGGGCAGGGAAGGACTGGGCCAGGGCAGGCTGGGAGATGATGATGTCTTC
TGTGCTCTGGGCCAGCAGGACTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACTG
AAAGACAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCCAGGGA
AAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDATVNK
IALELCTFTLAIALGAVLLLLPFSIISNEVLLSLPRNYIYIQLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYPYLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWPLDMLLHRQVLALQTRVLLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFAVIQVVLIFYLMVSSVVGFY
SSPLFRSLRPRWHDAMTQIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDGFRFNWLGNFY
IVFLYNAAFAGLTTLCLVKTFTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

000001-1101

GGCTGCCGAGGGAAGGCCCTTGGGTGGTCTTGGTTGCTTGGCGGCGCGGNTTCNTCCCC
GCTCGTCTTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCATATTCGCCAGAGAGGATCCGCGAGTGTA
TTATATCAACACTTGTGTTTGCAACACTGTACATCTCTGCACAGATCTTCTGACCCGCTTC
AAGAGCCTGCTGAGTTACACACAGCTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTGTGTCNTCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCTTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCATGCTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCA GTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCCAGAAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCCTGGCATTCCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCCCTCACAGGCCGGGTGGGCTGGCGAGCCGACGCGGGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCCGTGATGATCCACAAGCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA
 GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTCACACTTCTTTGGGGATT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAAACGGAAGTGCAATTGTCGGCAAGAGAT
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTACGGTTCGGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACCTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTCATTGCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTTAGCAATTTCAATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTGT
 TTATTTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDFQ
 AQEKFQDLGAAYEVLSDSEKRRQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGT PRQQ
 DRNIPRGSDDIIVDLLEVLTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
 MTQEVVVCDECPNVKLVNEERTLEVEIEPGVRDGM EYPFFIGE GEPHVDGEPGDLRFRIKVVVKH
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHK VHSRDKITRPGAKLWKKGEGLPNFD
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

TGGGACCAGGGAACCCGGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGNGTGCACCGAA
CGCGCGGGCGGAGGAGGTTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCANTTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCGTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTGAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAGAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGTTTCATGTTTGAGGAACCCCTNGTCAGCAAGACAGA
AATATCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGGAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGACTGAGTCAGGAGCCCTCTGGAAGCATGG
AGACTGTGGTGATTGTGGCATAGGTGTGCTGGCCACCATTCTTCTGGCTTCGTTTGCAGCC
TTGGTGCTGGTTTGAGGCAGCGCTACTGCCGCGCGAGACCTGCTGCAGCGCTATGATTCT
TAAGCCCATTTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
GAAGATGCCCTCGGTCTCATGTCCACTGCATTGCCATCTTGAAGATTTGTCACTCTGAC
AGAGAAGCTTGTGGCATGACAAATGGGCTCTGGGGCCAAAGATGAAGACTTCAGCCAGTGTCA
GCGACATCATTTGGTGGCCAAGCGGATCAGCCCCAGGTGGATGATGTTGTGAAGTCGATG
TACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACACTGCCCTGCTCCTGTCTGTGAG
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
AGTCTCTGTGCGCTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
CCAGATAAAGGCCTCCAGGCCCTGAAGGCTTCTGCAGGAGCAGTCTGCAATTTAGTGCCT
ACAGGCCAGCAGCTAGCCATGAAGGCCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCCTT
CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
TAAAGCAGGAGATCCCCGTAGTTTATGCCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGT
GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
CTGGTGGACTGTCAGCTTTATTAGCTCACCCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
AAGAAATCAAGAGGTTTCACATTAAATAGAAATTTCTGGCTCTCTCGATCGGTGAGAAATG
TGTGGCAATTTGATCTGCATTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
TTCTTTTGGCAAGACTTGACTCTCTCACCTGGCCTGTTTCATTATTGTATTATCTGCCT
GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGGTTTGGGTTTGAAGCTGAGGAAC
ACAAAGTTGATGATTTCTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

0992521-11401

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIALKICHTLTEKLVAMTMGSGAKMKTSA
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
2193
2194
2195
2196
2197
2198
2199
2200
2201
2202
2203
2204

FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCACCCCTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCC
 CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTCTGTCTTTTGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATTGGTTTGAAGAAGAACATTTCAGAT
 TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTGTAGTC
 CTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAG
 GGGCTTCTTCTGTGCTTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA
 AGTGAATTTGAAGACTCATTAAAAATATTGTGTATTATATAAAGTCATTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAAGTCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTGTGTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCGTTTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTGTGCT
 TTTTAGAAGTGTCACCTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTAAAGTATTAAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTGNGCNAGGGCC

FIGURE 90

MISLTDQTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFLLFRGFFPVVVGFIIRVPVLGSLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTCTGTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

GGCAGCAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAT
GGCTGCCAGGAAGGAGACGCCTTCTCTGAGTCTGGATCTTTCTTCTCTGGAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGACCTCGCGGGACTGC
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTACGCTCTTCACTCTCCTCCTCTGGCCCATTAAACAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGTAGTCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAAT
GCCATCGTGGTCTCAACACAAAGTTTGAATTTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGTCTCTGGCCAAGAAAGAGCTGGCCTATGTCCCA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCGAGAATATTTTTCTT
GATTCAGTGTAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGAGTGGCC
GGGCCAGGGGCTGCCCTCGCTCAAGCATACCTTTGTGCCAACCAAGGGCTTCGCCATC
ACCGTGAGAGCTTTGAGAAATGTAGTTTACGCTGTATATGACTGTACACTCAATTTAGAAA
TAATGAAATCCAACACTGCTGGGAGTCTTAAACGGAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGTCTCGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCGAGA
GACGCCCATGGTGCCCCCGCGCGCCCTGGACCTCTGTGAAGTGGTGTGTTTGGGCCTCGC
TGGTGCTCTACCCTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTACGGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTGTAACTTT
TTTTCCCCATGTGCTTTAGTGGGCTTTGGTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAAGTGTGAACCTTTGTTCTGTGATCATAGAAAGGCTATTTAGGCTCGAGGGAG
GGCAGGGCTGGGACCGAAGGGGACAAGTTCCCTTTTCACTGCTTTGGTGTGAGTTCTGTG
AACCTTTGTGTTGCCAGAGATAAGGTGAAAGTGCCTTATAGTGAGATGACTAAATTTATGCCTC
CAAGAAAAAAAATTAAGGTCTTTTCTGGGTCAAAAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIAAGLIINTIQLFTLLLPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGSKVLAKK
ELAYVPIIGMMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHHLLPRTKGFATVRSRLRVVSAVYDCTLNFRNNENPTLLGVNLGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

000001-123260

FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACTCAACACGGACTCGGACACGGAAGGTTTCTTCTTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTAGCTTTTATAAATCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAAATGTGGTAGGT
 TGGTACAAATTCCGTCGTCATTAGATCAGATCATGACGTTTAGAGAGAGGGCTGCTTCACAA
 AAACCTGACAGGAGCATTTTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTATATAAAC
 TGTATCAGGTTCCGTGATGTCCACTGGTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAGGATGTAACACAGATTAACCGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAATCCAAAAAGACCTCAGGAGAACATTTTCTTGTGTCAGGCATTA
 CGGACCTTTTTTCCAAATCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAATAGACA
 TGTTCATAAAGTAGCTGTAACACCAACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATCAAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATCTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTT**TGA**TCTTTTTAACCTTACAAGGAGATTTTTTATTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGACAGTAAGTTTCATTGTTTTTACTATGTTAC
 CTGTTTGACAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAAACCTTTTTTACCTTTCTACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATCTTTAGAATTGGAAGGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATTGCTATTAAAAATAAAATGGAAAAGCAAGAATAGCCTTAT
 TTCAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAAATTTAAAAAAAAAAAAAAAAAAAAA

MEGESTSAVLSG FVLGALAFQHLNTDSDTEGFLLGVEVKGEAKNSITDSQMDDVEVVYTIIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRHRSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTRLEHSLYKPQKGLFHRVPLVLANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMVEHTDIPEASPSTPQIIKHKALDLDDRWQFKRSRLDQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMGKGFGEYSRSPTF

FIGURE 96

GGCACAGCGCGCGCGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACACGCGCAGGGCAGC
 CCAAGCAGCGCGCAGCGAAGCCCCCGCGCCACACCCTCTGCGGTCCCCGCGCGCCTGCCACCCCTCCCT
 CTTTCCCCGCGTCCCCGCTTCGCCGGCCAGTCAGCTTGCCGGTTGCTGCGCCCGGAAACCCCGAGGTCACCA
 GCGCGCGCTCTGCTTCCCTGGGCGCGCGCGCCTCCAGCCCTCTCTCCCCCTGGCCCGCGCTGGCACC
 GGGGACCGTTGCTTGAAGCGAGGCCAGCTCTACTTTTGGCCCGCGCTCTCTCCGCTGCTCGCTCTTCCAC
 CAACTCCAACCTCTTCTCCTCCAGCTCCACTCGTAGTCCCCGACTCCGCGAGCCTCGGCCGCTGCCGTAG
 CGCGCTTCCCCGCTCCAAAGGTGGGAACGCGCTCCGCCCGCGCCGCACTGGCACGCTTCGGCTTGCC
 CGCGCTTCTCTGCACCTTGGCAGTGCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAGTTGCTCGG
 AAGTCGCGAGCTCTTACGTGTCCAAAGGCTTCAACAAGACGATGCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGCCCCAGGGTTACCTGCTGCTCTCAAGAGATGGAGGAAAGTACAGCTTCAAAAGTAAAGA
 TGATTTCAAAGTGTGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTACGTTACAAAGAGTTT
 ATGAATTTCTCAAAGAACTACTTTGAAAATGCAGAGAAATCCCTGAATGATGTTTGTGAAGACATATGCCAT
 TTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACTGGAAAGAAATGCTAAATGACTTCTGGGCTCGCCTCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAATTTGAAGCTCCAGGTTACTCGTGCTTTGTAGCAGCCGCTACTTTGCTCAAGGCTTAGCGGTTGGGG
 AGATGTGTCGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGCTCTGTGACTGTGAAGCCATGTTACAACCTACTGCTCAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCCCTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATAATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGAACCCCCAACGCCCCCTCCAGCTGGACGAAT
 TCTCGTTCATCTCTGAAGTGGCTTCACTGCTCGCTTCAGACACATCACCCGAGGAACGCCAACACACAGC
 AGCTGGCCTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTCAACACAGGCCAAGAAATTTCTGGTCT
 CCGCTTCGAGCAACGTTTGAACGATGAGAGGATGGCTGCAGGAACCGCAATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACTGTTTGCAGTGACAGGAAATGGATTAGCCACACAGGGCAACACCCAGAGGTCCA
 GGTGTACACACAGCAAAACAGACATACCTGATCCTTCTGCAATCATGGCTCTTCGATGATGACCAAGATGA
 AGAATGATACAAATGGGAACGAGCTGGACTTCTTGATATCAGTGATGAATAGTGGAGAAGGAAGTGAAGT
 GCTGTGAGTATCAGCAGTGCCCTCAGAGTTTGACTACAATGCCACTGACCATCTGGGAAGAGTGCCAAATGA
 GAAAGCCGACAGTGTGCTGCTGGGTCAGGCGCTACCTCCTCCTGCTCTGTCATCTTGTCTCTCGG
 TTATGCAGAGAGTGGAGATTAATCTCAAACCTCGAGAAAAGTGTTCATCAAAAAGTTAAAGGCACCAAGT
 ATCACTTTTCAACATCTAGTGACTTTCCTTTTAAATGAATGGCAACAAATGTACAGTTTTTACATATGGC
 CACTGTTTTAAGAAAGTGCAGCTTTGTTTTCTCATTAGTTTGGGAGGAAAGGACTGTGCAATGAGTTGGT
 TCTGCTCCCCCAAACATGTTAAAGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCAATTTGTGA
 TTTTATCACTCTATTATTTGTTGTATGTTTTTCTCATTTCGTTTGGTGGTTTTTTTTCGAAGTGTGATCT
 CGCCTTGTGTTTCAAGCAAAACGGGTCCCTCTGGCAGTAACATGTACGTATTCTGAAATATTAAATA
 GCTGTACAGAAGCAGGTTTTATTATCATGTTATCTATTAAAGAAAAGCCCAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLVMQNSSELFKDLEFVELKRYVVGVNLEEMLNDFWARLLERMFLVNSQYHFTDEY
LECVSKYTEQLKPFPGDVPRKLKLVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNFNIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQGCPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCCATGAAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAAATTCATGACAGTGTCTGGGCTGCCAAGAAGC
AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTCTCCACCTCCTCTCCACTGTACCCACC
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGTGCTCTC
TCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTCAATTTAACCTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

99/330

FIGURE 99

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

090221.4404

FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCTCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAAACAGAACTCATTTTGAAACCC
CTGACTGCATTTTGGCTTTTAGAAAGTTAGAATAAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

101/330

FIGURE 101

MAVLVLRLTVVLGLLVLF LTCYADDKPKDPDDSGKDKPDPDFPKFLSLLGTEIIENAVE
FILRSMRSRSTGFMEFDDNEGKHSSK

000000.000000

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCACTCCTGCAGCTGCTGGTGTCTGCTTCTTAC
 CCTGCCCCTGCACTCATGGCTCTGCTGGGCTGCTGGCAGCCCCGTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTCTGTCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTTATGTGGCAGCAAGTTTTCGAGCCCACTGGAAACACATTGGGGATGGCTG
 CTGCCCTACCCAGAGAGACCTGGAAGGATCTTGAGAAGCCCAAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTGTCTCTTCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACC**TAG**CAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAGAGCTCTACTTCTACGCTGACCAGGGAGGAAACACTAGGACCC
 TGTGTATCCTCACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
 CTCTAGGAAGTGGTCAAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT
 CTCCCCACTACCCTTCTTCTCTGAGCTGGGGGCACAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

FIGURE 103

MDILVPLLQLLVLLLTPLPHLMALLGCWQPLCKSYFFYLMAVLTPKSNRKMESKKRELF SQI
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLT K SMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRVLRPGGV LFFWEHVAEPYGSWAFM
WQQVF EPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGP HIMGKAVKQSF P
SSKALICSFPSLQLEQATHQPIY LPLRGT

103/330

GTGGGATTATTATTAGTGC AAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAG
CAGATGTTGGGGCTTTGTGCCAAGAGCTCCCCCTGCGCAGCTTCTGTAGATAAGGGTTAA
ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTG
TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
TTAAGGAATGAGGTTACAGATTGAGGAATGTAGGGCTCAACCTATAGACTTTGTCCCAA
TGCTCTCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
AAGACAGGCTTGGGGGGGCCATTGACGCTATAAACAGCATTGAGCACAACACTCGCTCCAAT
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAG
TGATTCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCATAAECTTTTGAAGGAA
AAGTAAAGGAGGATCTGACCAGGGGGAATCCATGAACCTTTAACCTTTGCAAGTTCTAC
TTGCCAATTTCTGGTTC CAGCGCAAGAAGGCCATATACATGGATGATGATGTAATTTGCA
AGGTGATATTCTGGCCCTTTACAATACAGCATGAAGCGAGACATGCAGCTGCATTTTCAG
AAGATTGTGATTCCGCTCTCATTAAGTTGTCACTCCGTGGAGCAGGAACACAGTACAATTAC
ATTGGCTATCTTGACTATAAAAAGGAAGAATTGTAAGCTTTCCATGAAAGCCAGCACTTG
CTCATTTAATCCTGGAGTTTTTGTTCGAAACCTGACGGAATGGAACGCAGAGATATAACTA
ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTTGCT
GGTAGCATCACACACCTCCTCTGCTTATCGTATTTTATCAACGCACTCTACCATCGATCC
TATGTGGAATGTCGCCACCTTGGTTCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA
AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCATGGGGGAAGGACTGCTTCATAT
ACTGATGTTTGGGAAAAATGGTATATTCAGACCCAACAGGCAAAATTCACCTAATCCGAAG
ATATACCGAGATCTCAAACATAAAGTGAACAGAAATTTGAACGTGAAGCAAGCATTCTCTCAG
GAAGTCTTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
GCAAGCCATGGA AAAAGATGTGTCAGCTAGGTAAGATGACAACTGCCCTGTCTGGCAGTC
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTT
ACTACAATGCTGAATGACTGGAAGAAGAACTGATATGGCTAGTTGCACTAGCTGCTGACAGA
TAATTCAAAATGCTGTTGGTTTTAAATTTTGTAACCTGTGGCTGATCTGTAATAAACTT
ACATTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIGHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRONITNQLEKWMKLNVEEGLYSRTLGSITTPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKAAKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

FIGURE 106

TGGTTTTTGCCCCATAAATCCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTACGCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGCGGGTTCGGGGCGGGGTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACCGGGGTGTCTCTGAGCCTGGTGGGATCCCGGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTACGACACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCTTAACTTTTGAAGGAAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCAGCGCAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGGAACGACAGAATATACTAACCACCTGGAATAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCCTGGCTGGTAGCATCACACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGCCGCCACCTTGGTTCCAGT
 GCTGGAACCGATATTACCTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATCCA
 GACCCAACAGGCAAAATCAACCTAATCCGAAGATATACCGAGATCTCAACATAAAGTGAAA
 CAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAGATAGCATGCGTGGGAAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAAACCTGCTGTTGGTTTTAATTTT
 GTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTCAATAGGTAAAAAAGAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCTGCTGTCATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCTGTCTGAGAAGGCCCCACCACCCAGAAGCCAGCCATGAAGGCAGCTACCTGC
TGCAAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGCTTATGAGTTGGTGTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCCTGGTCTCCAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
AAAAAAAAAAAAAAAA

0000000000

FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGGAA
 TC**ATGT**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTCTCAGAAAGAGAATAAAAT
 GACAGTTGAGCTTTTCCAAATCACAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCCAGGTTATGGAAGCGGCCAAAGTGGAAATATAAGCCCC
 TTCGGGCATTTCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTC
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
 AAAAAATGATCCTCCTGATCATCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATGTGCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAAGTGTCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTTCAAGAAGTCAAGTCACTTTACATCTATTAAGTGTCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAAGTACAATCG
 GGCAATCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACCTTTTCTGTGTTTTGCTGTGTAGT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGGAACAGAACTCCAGGCCATTGTGAGAT**TAGAT**ATACCATTTAGGTATCTGTACCT
 GGAAACATTTCTTCTAAGAGCCATTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTAAAGACCTAATAAACCCCTATTCTCTCTCAAAA

MSGRDITILGLCILALASLAMMFTFRFITLLVHIFISLVILGLLFCVGLWWLYDYDNDL
SIELDTERENMKCVLGAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFFWLVWAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWVAPLLLVAFAYLVAH
SFLSVFETVLDALFLCFVDLETNDGSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTLEQAIVR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCTT
 AGAATAAATTTGTATGGGATTTGTGATGCAGGAAGCCTAAGGGAAAAAGAAATTCATTCTG
 TCTGGTGAATAATTTTGGAAAAAAATTCCTTCTTCAAAACAAGGGTGTCAATTCGTATATT
TATGAGGACTGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCCCTGTTTTGCTGTG
 TCACCTGGAGTACATTCAACAAGAAACGGCAAGAGATTAAAGAGCCCAAGTTCACTGTG
 CCTCAGATCAACTCGCATGTCAAAGCCGGAAAGATCATCGATCCTGAGTTTCATTTGTGAAATG
 TCCAGCAGGATGSCAAGACCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACT
 CCAGTCTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAAGAGGGAATACTTT
 GTTCSGAAGGTTGCTGGACAGTCTGTTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTT
 ATCCCTACCCAGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAA
 CCTACCATCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGGTGAGACC
 CCAAAAGCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCACTTGCCAAGGCCATCCCCCTCTG
 CTGCTTCTACCCAGCAGTCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACTACACAAGCAGCAAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCCAGATCCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGCGGATGTCAGCCTGGGAC
 TTGTTCCAAAAGAAGAAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATTGACTTGTCTGTTTTAATTGATGGGAGCACCACTGATTTGGCAACGGCGATTCCG
 AATCCAGAAGCAGCTCCTGGTGTGATGTTGCCCAAGCTCTTGACATTGGCCCTGCCGTTCCAC
 TGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACACACAGC
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGCTCGGGCCATCTCCTTTGTGACCAGAAGTCTTTTCCAAAGCCCAATGGAAACAGAGGG
 GGGCTCCCAATGTGGTGGTGGTATGGTGGATGGCTGGCCCAAGGCAAAAGTGGAGGAGGCT
 TCAAGACTTGGCAGAGAGTCAAGAAATCAACATTTCTTATCACCATTGAAGTGTGCTGTGA
 AAATGAGAAGCAGTATGTGGTGGAGCCCAACTTTGCAAAACAGGGCGTGTGCAGAACAAAGC
 GCTTCTACTCGCTCCACGTGCAGAGCTGGTTTGGCCCTCCACAAGACCTTGACGCTCTGGTG
 AAGCGGCTCTGCGACACTGACCGCCTGGCCCTGCAGCAAGACCTGCTTGAATCGGCTGACAT
 TGCTTTCGTATCGACGGCTCCAGCAGTGTGGGGACGGGCAACTCCGACACCTCCTCCAGT
 TGTGACCAACCTCAGCAAGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCGGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTTCGACAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGTTGGCTACTGGAGTGGTGGCAGCAGCAGGGGGCTGCCATCA
 ACTTCGCCCTTGAGCAGCTCTTCAAGAAGTCCAGGCCCAACAAGAGGAAGTTAATGATCCTC
 ATCACCAGCGGAGGTCTACGACGACGTCCGGATCCAGCCATGGCTGCCCATCTGAAGGG
 AGTGTATCACTTACGATAGGCGTTGCCCTGGGCTGCCCAAGAGGAGCTAGAAGTCATTGCCA
 CTCAACCCCGTAGAGCACTCCTTCTTTGTGGACGAGTTTGACAACCTCATCAGTATGTC
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTACAGAG
 CAGGCAGAGCACCAAGCAGTGTGCTTTACTAACTGACGTGTGGACCAACCCACCGCTTAA
 TGGGGCAGCAGCGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAACAAATGTCTGTTATTA
 TTCTTTGCTATCATCTCTTTTATATTCCAAAACCTGGAGTTACAAAGATGATCACAAACGT
 ATAGAATTGAGCCAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGACAATT
 GTTCTTCAAAATTAATTTGCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTAAAGTTGTTATTTCTGATTTGAACCTCTGTAACCCCTCAGCAAGTTTTCATTTT
 GTCATGACAAATGAGAAATTGCTGAATTAATGTTTGAAGGATGAAAAATAAAAAATAAAAA
 AA
 AA

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTVGVHSNKETAKKIKRPKFTVPQINCVDKAGKIIDPEFIVKC
PAGCQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL
SLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVVTLMO
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGSAAFQKPVGADVSLGLVPKEELSTQSLFVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHTNLKTHTNLKTAEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTDRACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKFEISDTDRIGAVQYTYEQRLEFGFDKYSSKPDIL
LNAIKRVGYWGGTSTGAAINFALQLEFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSEFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

CAGAGTGAACGTGGTTGACGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTA
TGCCCTTTCCGGCTGCTCATCCCGCTCGGCCCTCTGTGCGCGCTGCTGCCTCAGACCCATTGGT
GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCCGCCACTACAGTTTTTCTCTGACTCTAAT
TGATGCACCTGGACACCTTGCTGATTTTGGGAATGTCTCAGAATTCAAAGAGTGGTTGAAG
TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGAAACAAACATT
CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAGTAGA
GGCTGGATGGCCCTGTTCCGGGCCCTCTCTGAGAATGGCTGAGGAGGCGGCCGAAACTCC
TCCCAGCCTTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACTTACTTTCATGGCGTG
AACCAGGAGAGACCCCTGTCACTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
CACCTGAGCAGCCTCACTGGTGACCCGGTGTTCTGAAGATGTGGCCAGAGTGGCTTTGATGC
GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
AAGTGGGTGGCCAGGACGCAGGCATCGGGCTGGCGTGGACTCTACTTTGAGTACTTGGT
GAAAGGAGCCATCTGCTTCAGGATAAGAAGCTCATGGCCATGTCTTCCTAGAGTATAACAAAG
CCATCCGGAACTACCCCGCTTCGATGACTGTCGTTACTGTGGGTTTCAGATGTACAAGGGGACT
GTGTCATGCCAGTCTTCAGATTCCTTGGAGGCCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
CTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCACCCCT
CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGGCGGAT
TTGCAACAATCAAAGATCTGCGAGACCACAGCTGGACAAACGCATGGAGTCGTTCTTCTCTG
GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCCAACCAACTTCATCCACAACAATGG
GTCCAACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGGTACA
TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTTACTCTCTCAAACGAGGACGGTC
GAAATTTTCAGAAAAACACTGTTAGTTCGGGGGCAATGGGAACCTCCAGCAAGCCGAGGAACAC
TCTTCTCACCAGAAAACATCAGCCAGGCAAGGAGGAACTGCCAACACAGAAGTCCCA
CTTCTCAGCTGCCCGGATGACCCCTTCACTTCAAGTTGGCATTACTGGGACAGGTTTTCTCT
AGACTCCTCT**GA**CCACTGGATAATTTTTTTATTTTTTATTTTTTGGGCTAAACTATAATA
AATTGCTTTTTGGCTATCATAAAA

MPFRLLIPLGLLCALLPQHGHGAPGPDGSAADPAHYSFSLTLIDALDITLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKI
LPAQQTPTGMPYGTVNLHGVNPGETPVTTAGIGTFFVEFATLSSTTGDVPFVEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWAQDAGIGAGVDSYFEYLKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMMPVQSLEAYWPLQSLIGDIDNAMRTFLNYT VWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLRATGDPITLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMRESFLLAETQVLYLLFDPTNFIHNNGSTFDVAITPYGECILGAGGY
IINTEAHPIDLAALHCCQKRLKEEYKVEDLMREFYSLKRSKFKQNTVSSSGPWEPPARPQT
LFSPEHNDQAREKPKAQKVPLLSCPSQPTSKALLGOVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAAGTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGTTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
ATGCAGACTTTCACAATGGTTCTAGAAAGAACTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTCGAATACCAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCAGTGTGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCAGAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTGTGGCCTACTGGAGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTGTGTGGCTTCATGCTGATCCTGT
 GGTCTGCCACTGTTCTGCTGGAAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCCAGACACCTTGAATAACCAATTCACCCAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCTGTGCCACGGCTGTGATGTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCATAGGTTTTGCGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGAGAGAGCCACTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGCTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTCAAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTGTTAAAGTACAGAATTCAGCAATAAAAAGGGCCACCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

MQTFMTVLEEIWTSLFWFFYALIPCLLTDEVAILPAPQNLVSLSTNMKHLMLMSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLSTEGPECDVTDITATVPYNLRVRATLGSQTSAW
SILKHPFNRNSTILTRPGMEITKDGHLVIELEDLGPQFEFLVAYWRREPAAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVVEVQGEAIPVLVLAFAFVGFMILIV
VVPFLVWMKGRLLQYSCCPVVLPDCLKITNSPQKLI SCRREEVDACATAVMSPEELLRAWIS

Signal peptide:

amino acids 1-29

amino acids 230-255

amino acids 40-43 and 134-137

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTACGGCTTCGCTGCGACTAGACCTCAGTCCAACATATGCA
TTCCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCATGTTTGCTCAGAGATGAAGTGCCATTCTGCG
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTAATACTTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTCTGAGTGTG
ATGTCACTGATGACATCAGGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATATGGGC
TCACAGACCTCAGCCTGGAGCATCTCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCNCCAGTTGAGTCTCTTGTGGCTANTGTGAGGAGGGGCGAACCCTTGCGGCGCAAGG
GTNNCGCAACCCCTTGGCCGCGCTGGGGTATTGCTGAGAGAAAGGAGGCCCAATATGACCCAC
ATACTCAATATGGAGCGAANTGCTATTGTCCACCTGTTTGTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCCATGTGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCGCAGCAGGAGCAGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCTGAGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCACCTACAGTGTCTCATTTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGAAAAGG
 TGGTAGGGGCTTGGGACCAACTGTGTGCTAGTGGAGGAGGTCAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATTAACCACCGCGTCTCCTCCTCCACCA
 CCTCATCCCCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG
 AGACCCACTGACTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
 AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTGCATATAAACCAAAAAATAACTTGTATTCAAT
 AAAAATTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTGTGTT
 GTTATTTCTCTGTATTATTTTCTTATTACAAAAGAAATGCAAGTTTCAATTGTAACAATCCA
 AACAATACCTCACGATATAAAATAAAATGAAAGTATCCTCCTCAAAA

[illegible]

FIGURE 120

MVAATVAAAWLLWLAAACAQQEQDFYDFKAVNIRGKLVSLSEKRYGSVSLVNVVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFCNQGQEQEPDSNKEIESFARRTYSVSPFPMFSKIAVTTGTG
AHPAFKYLAQTSKGKPTNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKILLKREDL

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCGAGGGCAAAGCGAGCC**ATGG**CTGTCTACGTCGGGATGC
 TGGCCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGTTGCGAGGGTGTCGCTTCCCTCAGTTCACAGAGAGTGGATCG
 CATGGTCTCCACGCCCATCGAGGCCCTCAGCTACGTTCAAGGGTGACACCAAAAGCATCTTA
 ACAGCAAGACTGTGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAAGACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTACAGTTGACCTTTGGCCAACTCAAGGAGGAGTGGACAA
 AGCTGCTTCTGGCCCTCCTGAGCATTGGCCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAACCTGGAGTATGCCTCAAGAAGTGGGCTGCAA
 GGCCCTTGTTGCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGGACCTGCTCCTGGATGAAGTGGTGCCGG
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCCTGTCTGCCATG
 ACCCATCAACATCCAGTTCACTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACATCAACATTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAG
 GCACAATGATGTGCTGATGTACGGTGCCACCTCATCTGCGCTCTCCCATCTTCAATGGC
 AAGAAGGCACCTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGTTACCCCAAGAT
 GTTCGTGGACATTCTGAACACGCCAGACTTCTCCAGTTATGACATCTCGACCATTGTGGAG
 GTGTCTATTGCTGGGTCCCTTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAACAGTCCCGTGACATTGCGGCACCT
 CCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCTCACACGGAGG
 CCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACAGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTCAGGTTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCTGCATTCCGGCTGAAGGACGGGGAGGAGACCAGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCAAACTACCCCTCACCATTTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCCCTGCTGGCCGGTTGGCTT
 GACTCTCTCTGTGCAAGATGCAACCTGGCTTTATGCACCTAGATGTCCCAGCACCCAGTTG
 TGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAACCTAAGAGCTCCTGGATGGGTC
 CGGGAACCTCGCTTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCTGT
 TCCATCCCCACATTCCCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTCTTT
 GAAAAAAAAAAAAAAAAA

MAVYVGMRLRLGR LCASSGVLGARAALSRWQEARLQGVRLSSREVDRMVSTPIGGLSYVQ
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPNYSYAWVLMQLATAQAGIILVSNPAYQAMELEYVLKKGCKALVFPKQFKTQOY
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLDEVVAAGSTRQHLDDQLQYN
QQFLSCHDPINIQFTSGTGTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGVIAGSPAPPELLIRAIINKINMKDLVVAYGTWENSEPVTFAHFEDTVEQKAESVG
RIMPHTEARIMNEAGTFLAKRLNTPGELCIRGYCVMLGYWGEPOKTEAEVDDKQKWTGDVAT
MNEQGFCKIRVGRSKDMIIRGENGIYPAELEDFFHTHPKVQGVQVGVQKDRMGEETCACIRL
KDGEETTVEEIKAFCKGKISHFKIPKYIVFTVNYPLTISGKIOKFKLREQMRHLNL

amino acids 1-22

amino acids 140-161, 213-229, 312-334

amino acids 260-271

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACCTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGTGGACATTTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

GAGCAGGACGGAGCG**CATG**GACCCCGCCAGGAAGCAGGTGCCCAGGCCATGATCTGGACTGCG
AGGCTGGCTGCTGCTGCTGCTGCTGCTGCTCGCGGAGGAGCGCAGGCCCTGGAGTGTCTACAGCTGCG
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GC CGCGCGG
GTGGACGTCTGTCACCGAGGCCGTGGGGGGCGGTGAGACCATCCACGGACAATCTCTGCTGGC
AGTGC GG GGTTCGGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGG
TTCTGGCGTTTCATCCAGCTGTCAGCAATGCCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTG
CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCGCGCGTCTGTGAGCT
GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACTTGTACGGCA
GCTAATGTGACTGTCTTGTCTGCTGCTCGCGGGCTGTGTCAGGATGAATCTGTGCATCGGGA
TGGAGTAACACGGCCAGGGTTACAGCTCAGTGGTCTCTGTTGCCACGGGTCCCGCTGTAAC
CTGACCTTCGCAACAGACCTACTTCTCCCTCGAATCCCAACCCCTTGTCGGCTGCCCT
CCAGAGCCACGAGCTGTGGCCTCAACCACATCTGTCAACCTTCTACCTCGGCCCAAGT
AGACCATCCACCACCAACCCATGCCAGCGCCAACCAAGTCAAGTCCGAGACAGGGAGTAG
AACACGAGGCCCTCCCGGATGAGGAGCCAGGTTGACTGGAGGCGCCGTGCGCACCAAGGAC
CGCAGCAATTGAGGCGAGTCTCTGCAAAAGGGGGGCCACAGAGCCCAATAATAAGGCTG
TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCGTGGCTGCTGGTGTCTACTG**T**
GAGCTTCTCCACCTGGAAATTTCCCTCTCACTACTTCTCTGGCCTGGGTACCCCTCTTCT
CATCACTTCTGTCTCCACCACTGGACTGGGCTGGCCAGGCCCTGTTTTTCCAACATTCCC
CAGTATCCCCAGCTTCTGCTGCGCTGGTTTTCGGGCTTTGGGAAATAAAATACCGTTGTATAT
ATTCTGCCAGGGGTGTTCTAGCTTTTTTGAGGACAGCTCCTGTATCTCTCATCCTTGTCTC
TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAAGAGAGTCAAGTGTACGGGGAAGGTG
AGAGAGAGGATGCTAAGCTTCTACTCACTTCTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
GGTGGGTGGGACAATGGCTCCCCACTTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
GAATCGGTTCCCAATATGTCTTCTTACTAGACTGTGAGCTCTCGAGGGGGGGCCCGGTAC
CCAATTGCGCCCTATAGTGAGTCGTA

SECRET

MDPARKAGAQAAMIWTAGWLLLLLLRGAQAALCEYSCVQKADGDCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCSSGLPGKNDRGLDLHGLLAFIQLQQAQDRCAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDVGTGPGFTLSGSCCQSGRCSNDLNRKTYFSFRIPLVRLFPPEFTT
VASTSVTTSAPVRPTSTKMPKPAITSQTQRQVEHASEERPLTGAAGHQDRNSNG
QYPAKGGPQSPHNKGCVAPTKAGLAALLLVAAGVLL

[illegible]

127/330

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVQPSGGSLWNLRLLEPLDANVDA

000000.11401

AAACTTGA CGCCATGCAAGATCCCGGTCCTTCTCGCCGTTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCAGGAGGCCACCTGGGTGCTCTGAGGAAGAAAGCACCATTTAGAAATTATG
CGTCACGACCCGAGGCCCTTAAACACCCGTTCTCGAACATGCACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCCTTTCTTAAGCTGAAAGGACTGAGGAGCGCAACTCTCTGATGCCAGT
GCTCACTGACCTCCACTGGAAGAGGGGGCTAGCGTGAGGCGCTGATCTCAACCTACCATAACT
CTTCTTCGCTCCAGGAATCCCAATAAACATTTTCCATCCAAA

Science in the 19th Century

FIGURE 129

MKIPVLPAVVLLSLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPLFNWDAFPKLKGLRSATPDAQ

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTTC
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCACTATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTCTT
AAAAGTTTGAGTATATTTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

03992560

03992560

03992560

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCC**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTCTATAGAAGAGGATCTAATCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACCAG
 ATCCTCTCATTTCTGTCTCGGAAAAACCCAAACTTGTGTGATCGAGAATACACCAAAAAC
 CAGGCCTGGAATCTATGAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGCCATCTTGT
 GGATCACTGCAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCATATATCCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCCTCTTG
 AGTGAATACTCTAAATCTCTGTCTTATAATGTAACGAGAAGGAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACTGAATA**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGTCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACTGATATGAAGCAGTTCACTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG
 AAACCTTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCAATAAACTCTGTTACTCAG
 GAGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

090321-11401

MEWVASSPLRLWLLFLFLPSAQGRQKESGSKWKVFDIQINRSLNENYEPSSQNCSCYHGVI
EDLTPFRGGISRKMAEVRVRKLGTHYQITKNRLYRENDCMFPRSRCSGVEHFIFLEVIGRLPD
MEMVINVRDYPQVPKWEPAIPVFSFKTSEYHDMYPAWTFWEGGPAVWPIPYPTGLGRWDL
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD AEYTKNQAWKSMKDT
LGKPAAKDVHLVHCKYKYLFNFRGVAASFRFKHLFLCGSLVFHVHGDWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDDVAQEI AERGSQFIRNHLQMDDITGVYENWLLSEYSKFLSY
NVTNRKGYDOIIPKMLKTEL

FIGURE 134

CACCCCTCCATTTCTCGCCATGCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTCAG
 AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGACAGTGGTGATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCCTACCCTGGGACCGGACCGTCTCCTCCTTGCT
 TTCTCCTTACCCTCTACCTGGGCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATCTGAGTTTCAGCCA
 CTGAACCTCAAAGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCTGCACTGTTACTTGCCCTCTGCGCCTCAGGGGTCCCCCTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLIPAAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGFV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

CCGAGCACAGGAGGATTGCCTGCGTTTAGAGAGTGGCTGCGTTTGTGGGAAAAGCTATCAAGGA
AGAAATTGCCAAACCATTGCTCTTTTTTCTGTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
TTTAATTAGCATGGAATACAGAAAAACAACAAAACTTAAGCTTTAATTCATCTGGAATT
CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
AGCTGCTGTGGATGCGCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC
CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
ACAGACAAGACTTCACTTCACACTTCGAGAGCATTCAAACGTCTCTCATCAAAATCCATTT
CTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
TTGGGGTGAAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG
AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTCTAGAGGATGAACACCTTCTTTATGGT
GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAAACCATTATGGC
ATTCAGGTGGGTAACTGAGTTTTGCCCAATGCCAAGTACGTAATGAAGACACACTGATG
TTTTCACTCAATACCTGGCAATTTAGTAGAAGTATCTTTTAAACCTTAACCACTCAGAGAAGTTT
CTTCACAGGTTATCCTCTAATTGATATAATTTCTTATGAGGATTTTACCAAAAAACCCATAT
TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTATATATA
TGTCACAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAACCAACCATTCAAGTTT
GAAGATGTTTATGTGGGATCTGTTTGAATTTATTAAGGTGAACATTATATCCAGAAGA
CACAAATCTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTGGCAGGTCATGCTAAGGAACACC
ACATGCCATTATTAACTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
GTGTTAAATAAAGTAGGTACTGTGAAAAATTCATGGGAGGTCAGTGTGCTGGCTTACACTG
AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATAGTC
AGGCCCTTCAAGATGATATGTGGAGGAAATAATATAAAGGAATTGGAGGTTTTTGCTAAA
GAAATTAATAGGACAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTG
AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
TGTAGTTCGTGTCAAAAACCTTCTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
CATCTTTTACATGCAACATTTTCCAGTTACTTAAGTCAAGTTTTATTATTGATACATCAC
TCCATTAACTGAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTGGACTTTGTTAAAT
ATTTTACTGTGGTAATATAGAGAAGAATTAAGCAAGAAAATCTGAAA

1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Index**
 10. **Table of Contents**

MASALWTVLPSRMSRLSLKWSLLLLSLSSFVMWYLSLPHYNVIERVNWMYFYEYEPFYRQD
FHFTLREHSNCSHQNPFVLVLVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQBAEK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTCLKTMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPFYCSGLGYIMSRD
LVPRIYEMMGHVKPIKFEDVYVIGICLNLLKVNIIHPEDTNLFFLYRIHLDVCQLRNVIAHG
FSSKEIITVQVMRLRNTCHY

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACCGGTGGAGAACTTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGTTTTTACCATGTCAATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYINVNDDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQGKGPGGPPPKGLMYSVN
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTTCTGAAACTAATCGTGTGACAGAAATGACTTTGAAAAGCATTGCTTTTACAGAAGTATA
 TTAACTTTTAGGAGTAATTTCTAGTTTGATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAAATCGCATATGGTCCTAGTATTAATTTCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTAC**ATGA**ATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCGAGAGCTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCCGTTGCCAACTCGTCCCATTTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGAAAAAAGAAAGTAGAAAAAAGAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGGATGGAAGCTCAGCCCTTCAACCCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAAGCCCTTACAATGGTGTGAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGGCCCTCGAAGACATCATAATCAT
 GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAGAAGAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGTCCCTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAAACGCAAACTGATTAGGATTTGATTTCTTGAAACCCCTCTA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATCTGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATTGCAGACACTGTTCTATTAAAGTGGTTATTGTTTAAATGATGGTGAAT
 ACTTCTTAAACACTGGTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAAATACAAAT
 CTTGTTTTTTCTAAAAAAGT

MNDSLRTNVFVRFPQETIACACIYLAARALQIPLPTRPHWFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKKRVALEAKLKAKGLNDPGTALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASSPYNGVRKDKSRNSRNSASRSRSTRSRSHSPRRHHY
NRRSRSGTYSSRRSRSHSPRRHHNHGSPHLKAKHTRDLLKSNRHHGHRKRSRSRSQ
SKSRDSDAAKKHRRERGHHRDRRERSRFSRSHKSHHGGRSGHGRHRR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNNTATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAATTTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAGCAAGGGGATT
GAATCCGGATGGAAGTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

0002521.11401

GGACACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGACCCGCTTCTCGCACGCGTCA**TAGG**C
GGTCTCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCACCCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCGCTTCCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTCGCTTCTTCTCGGAGTACCAGTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGCGGTGTACCTCTTTCACAGAGGCCTACTACTACAT
GCTGGGACAGCCAAAGGAGACTAACATTGCTGTGTTCTGGTGCTGCTACCGGTGACCTTCT
CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTTCAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
GGAGGAGACCCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCGAACTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGGCTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCCTTCTGCACTTCCAGGCGCTCGCGCTGGC
CCAGACCCACCGGGAGCGCACTGACCATGTCGGAGGACAGACCCATGCTGCAGTTCTCTCTGC
ACACAGCTTCTCTGTCTCCCTGTTTATCTCTGTGGCTCTGGACAAAGCCCATTGCACGGGA
TTCCTGCAACGAGCGCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGGTTGCTGGTGGTGCTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCACTACCTGACGCGCTCATCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTTGGGGCCTGGGCGCCAGTCTCTTACTATCCCCGACCCATCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
GGCCCTGGGTGGCCTGCTTACTCCCCCTTCTCCTCGTGCGCTCTGGCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA
GGCTCT**TAGC**TGCCTGCAGACCTCTCTGGGGCCCTGAGGTCTGTTCTTGGGCGAGCGGACA
CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGCGGGTACTCCCC
GGCGTTCCCTTACCACAGTGCTGACCCGCGGCCCCCTTGGACGCGAGTTTCTGCTTCA
GAACTGTCTCTCTGGGCCCCAGCAGCATGAGGGTCCCGAGGCCATTGCTCCGAAGCGTATG
TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTTCTGTAACAAATAAAGGAGCATGCC
GATTTTAA

MAVLGVQLVVTLLTATLMLHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAFQLETCLPTTVDALVLRFFLEYQWVFDAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCCLLTVTFSIKMFLTVTRLFYSAEEGGRSVCLTFAFLFLLAMLVQV
VRETLELGLLEPGLASMTQNLEPLLKKQGWDAWPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPFLILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLLWLLVVLCLLRLAVTRPHLQGLCLAKARVEQLRREAGRIEARIQQRVVRVYCYVT
VVSLEYLTPLILTLNCLTLLKTLQYGSWGLGAPALLSPDPSSASAAPIGSGEDEVQQTARI
AGALGGLLTPLFLRGVLAYLWWTAAQCQLLASLFGLYFHQHLGAS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGNTTGGAGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

00054.1401

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCCGTGATTATTAAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAATTTCTTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTTGGTTTGGGCCCTTTAGCTTGACAGAAGGTGGCCAGGGAGAATGCAGCACATCTGCTCGGAGATGTAAGG
 CGCTCTGTGTGCTGGTCTTCGCTTGGCTCAGTCTCTGCTAACTACATTGCAATGTGGGCACCTGCACCTCTCTG
 TATTCAGAATCTGTAAAGTGCTCCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGCGAGCTCACAGCCAGGCTCCCTCCCCAGAGTTTCTGCAGCTGCCACCATCTCCTTTAA
 TGACAGACAGAGCTGGCTAGACACCCCTGCCCTACGTCTCTCGGCAGAGAGCGGCGAGTGCAGTTGCCAACCATGCCAGCAGG
 GTGGACTCTGGCCGGAGCAACCCGAAGTGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAAATAAATCGAGCTTTGAGTGTCTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCAGCAGG
 GCAGGGAAAATTCGAAAACACCCTGCCCTGAAGTCTTTCCAAGTTGTACCACTGATTCCAGATGCTGAA
 ATTACAGCATCAAGATCAATCGAGTAGATCCAGTGAAGCCCTCTCTATTAGGCTGGTGGGAGTAGCGAAAC
 CCCACTGGTCCATATCATTTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCTGCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCCGAGCAGGAACAATGGACAGGCC
 GGATGCTCAGACCCCGAGATGACAGCTTTATGTGATTTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACCTGGTGCAGAGTGGATGAGCCTGGGTTTTATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCATATGGCAGCCAGAAAG
 TGGCGGCTCATCTGATTAGGCCAGTGAAGAGCTGTTCACTCGTGTGCCGCAAGTTCGGCAGCGGAGCC
 CTGACATCTTTAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACAT
 CCCAAGCCCTCCATCCTACAATTACTTGTCTATGAGAAGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGAGGGGAGCATCACATAGAGAATGGGATTGCTATCTATGTCTCAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTTGTGAATGGATGGGGTCGAATGACA
 GAGGTGAGCCGAGTGAGGCAGTGGCATATTGAAAGAACATCATCTCGATAGTACTCAAGCTTTGGAAGT
 CAAAGATATGAGCCCGAGGAGACTGCAGCAGCCAGCAGCCCTGGACTCCAAACCAACATGGCCCCACCCA
 GTGACTGTTCCCATCTCTGGTTCATGTGGCTGGAATTACACCGTGCTTGTATACTGTAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTCTGCATTGTAGGAGGTTATGAAGAATACATGGAAAACAACTTTT
 TTTTCATCAATCCATTTGTTGAAGGAACACCGCATACAATGATGGAAGAAATAGATGTGGTGATATTTCTTGT
 CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGGTGGCAAGACTGCTGAAAGAACTTAAGGAAGA
 ATTACTCTAATATTGTTCTTGGCTGGCACTTTTTTATAGAAATCAATGATGGGTGAGGGAAGAACAGAAAA
 TCACAATAAGGCTAAGAAGTGAACACTATATTTATCTTGTGAGTTTTATATTAAAGAAAGAAATACATTTG
 AAAATGTGAGAAAGTATGATCATCTAATGAAGCCAGTTACACCTCAGAAAATGATTCCAAAAAATTA
 AAACCTAGTTTTTTTTTCAGTGTGGAGGATTTCTATTACTCTACAACATGTTTTATTTTTTTTCTATTCAAT
 AAAAGCCCTAAAACAACTAAATGATTGTTGATACCCCACTGAATCAAGCTGATTTAAATTTAAATTT
 GGTATATGCTGAAGTCTGCCAAGGTACATTTGGCCATTTTAAATTTACAGTAAAATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTTCATCAACCAAGAAATAATTTTTTCGAAGTTAA

000251.11401

FIGURE 147

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPPEVSA AATISLMTDEPGLDNPAYVSSAEDGQPAISPVD SGRSNRTRARPFERSTIRSRS
FKKINRALS VLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITS IKINRVDP
SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVP HNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQ LGIKLV RKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHD LRYGSPESA AHLIQASERRVHLVVS RQVRQRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKV VNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGV ELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELP RCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCCTCTCCCAGGCAAATGCTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTCAAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTATGTTTAGGATGATTAGCCCTCTGTTTTATCTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAAATTCCTTCCCAATGCCCACTAATTTTGAGATT
AGTCAGAAAATATAAATGCTGTATTATA

FIGURE 149

MKILVAFLLVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

149/330

FIGURE 150

GGCACGAGCCAGGAAC TAGGAGGTTCTCACTGCCCAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGCCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTTGAAGTTTCCCCAAAG
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
 CCACCTCAGGTGCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACCTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG
 AGCCAGACATCGGACTGGTTCCTGGTGCCAGGCTGCAACAACGCCAATGTCCAGCACAGCGC
 CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
 GCCCCATCCTTGCCCTGCGGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG
 GGGTTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAGCAGCAGCCATGTAGAATGAACC
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTGGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPPIITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

GGTCCCTTAATGCGAGACGCCGCCGTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
CTGTCCGGCTGGTCCCAGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCCT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCAACCTGTCACTGCCCTGGGGAAGAAA
CTAAATGTCAACAGCGCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTACAGCTGGAGAATTACACACCCAAGGAACCCCTCACCCTGC
AGGCAAGGATGCTTGTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTTCAGT
TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAAATGGACACAGCGTTCACTCC
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAAATGACAAGGTTGTGGCCATGCTCTTCATT
ACTTCTCAATGGAGACTGTATAGGATGGCTGTAGGACTTCTTGATGGGCATGGACAGCACC
CTTGGAGCCAAAGTGCAGGAGCACCACTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAG
GTCTTGATCAAATCGCCCTTCTGTCTGCCAGCTGCCACGACCTACGGTGATATGTCAGT
GGCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCTT
TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTCTTTCTT
TCTTTTGTTTGGAAATCAAGTACTTCTTGAATGATGATCTTTCTTGCAAATGATATT
GTCAGTAAATAATCAAGTTAGACTTACAGCTCTGGGATCTTTCCGTGCTGAAAGAG
AATTTTAAATATTCTTAATAAGAAAAAATTTATATTAAATGATTGTTTCTTTAGTAAATTTAT
TGTCTGTAAGTATTTTAAATTAAGAGTTCTATTCCAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVGGQVDEKTFL
HYDCGNKTVTFVSPPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEFLTQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVMAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAGAAAACCTCAAATTGGGAGGCCAAC
CCACAGAACAGCATTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTCTTTTGAAAAAAAAAAAAAAAAAAAAA

090257.11434

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHLEWLLIKREFGFYSKSYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

000000000000

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAAC**TGTG**CACCA**CCAC**CTGGAATGCCATCCTGCTCCCGTTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTTGCTCGTGCAGTAACCA**GTTCAGCA**AGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCTTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCGGACACCTTCCGCCACCTCCACACCTTGGAGGTCCTGCAGT
 TGGGCAGGAAC**TCCAT**CCGGCAGATTGAGGTGGGGGCC**TTCA**ACGGCCTGGCCAGCCTCAAC
 ACC**TGGAGCTGTT**CGACA**ACTGGCTG**ACAGT**CATCC**TAGCGGGGCC**TTTGA**ATACCTGTC
 CAAGCTCGCGGAGCTCTGGCTTCGCAACAACCC**CATCGAA**AGCATCCCTCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTT**GAGGGCTGT**CAACCTCAAGTATCTGAAC**TGGGCATGTG**CAACAT**TAA**
 AGACATGCCCA**ATCTC**ACCC**CTGGTGGGCTGGAGG**AGCTGGAGATGT**CAGGGA**ACCACT
 TCCCTGAGATCAGGCTGGCTCCTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCATG
 AACTCACAGGT**CAGCCTGATTGAGCGGA**ATGCTTTT**GACGGGCTGGCTT**CACTTGTGGA**ACT**
 CAAC**TTGGCCCA**ATAACCTCTCTTTGGCCCATGACCTCTTACC**CCGCTGAGGT**ACC
 TGGTGGAGTTGCATCTACACCACAAC**CCTTGGAACTGTGATTGTGACATCTGTGGCTG**AGCC
 TGGTGGCTTCGAGAGTATATAC**CCACCAATTC**CACTGCTGTGGCCGCTGT**CATGCTCC**CA**T**
 GCATGCGAGGCGCCTACCTCGTGGAGGTGGAC**AGGCCTCCTTCCAGTGCTCTG**CCCCCT
 TCATCATGGAGC**CACTCGAGACCTCA**ACATTTCTGAGGGT**CGGATGGCAGAACTTAA**GTGT
 CGGACTCC**CCCTATGTCTCCTCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCC**CAGC
 CTCCCGCAC**CAAGGATCTCTGTCTCA**ACGACGGC**ACCTTGA**ACTTTTCC**CA**CGTGCTG**C**
 TTT**CAGACCTGGG**GTGACATGCATGGTGACCAATGTTG**CAGGCA**ACTTCAACGCCTCG
 GCCTACCTCA**ATGTGAGC**ACGGCTGAGCTTAACACCT**CCA**ACTACAGCTTCTTCA**CCACAGT**
 AACAGTGGAGACCAGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTTA
 CCAGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCAGGTGCTCATTCAGACTACC
 CGTGTGCCAAGCAGGTGGCAGTACC**CGCGACAGAC**CACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCAC**AGCAGCGGAGTACAGTC**
 ACAGCCCGCCGGACTGTTGAGATAATCAGGTGGACGAAGACATCC**AGCAGCA**ACATCCG
 AGCAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCA**CAATTC**
 ATGACCATATTAAC**TACA**ACCTACAA**CCAGC**ACATGGGGCC**CACTGGACAGAA**ACAGC
 CTGGGGAACTCTG**CACCCACAGTCA**CCACTATCTGAACTTATATAATTCAGAC**CCA**
 TACCAAGGACAAAGTACAGGAACTCAAA**TATGA**CTCCCTCCCCCA**AAAACTATA**AAAT
 GCAATAGAATGCACAAAGACAGCAACTTTGTACAGAGTGGGGAGAGACTTTTCTTGTA
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAA**AAACAGATTATATTA**AAATTTAAAGA
 CAAAAGTCA**AAAA**A

090222.11401

MKLLWQVTVHHHTWNAILLFPVYLTAQVWILCAATAAASAGPQNCPSVCSNSQFSKVVCT
 RRGLESEVPQGI PSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
 LNTLELFDNWLTVIPSGAFEYLSKRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
 ISEGAFEGLFNLKYLNLGMCN1KDMPNLTPLVGLEELEMSSGNHFPFPIRPGSFHGLSSLLKKLW
 VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPDHLFTPLRYLVELHLHHNPNWNCDCDILW
 LAWWLREYIPTNSTCCGRCHAPHMHRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
 KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMPTNVAGNSN
 ASAYLNVSTAELNTSNYSFTTVTVTETTEISPEDTRKYKVPVTTSTGYQCPAYTTSTVLIQ
 TTRVPKQVAVPATD1TKMKQTSLEDEVMKTK1IGCFVAVTLAAAML1VFYKLRKRHQQRS
 TVTAARTVE1IQVDE1PAATSAATAAPSGVSEGAVALPTIHDHINYN1YKPAHGAHWTE
 NSLGNLSLHPTVT1TISEPY1IQ1THTKDKVQETQ1

FIGURE 158

CGCTCGGGCACCAGCGCGGCAAGGATGAGAGCTGGGTGCTGGACGAGTTGGGGCTCACTTTTCTTCAGCTCC
 TTCTCATCTCGTCTTCCCAAGAGAGTACACAGTCATTAAATGAAGCCTGCCCTGGAGCAGAGTGAATATCATG
 TGTCCGGAGTGTCTGTAATATGATCAGATTGAGTGCCTGCCCCGGAAGAGGGAAGTCGTGGGTATATACCAT
 CCCTTGCTCGCAGGAATGAGGAGAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAACT
 GCAAGAGCTGCCGAATGGCTGTGGGGGGTACTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCGAGAG
 TSCCGAGCAGGCTGGTACGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGGCCCAAGGGTTCAGATTTT
 GTTGGAAAGCTATCCCTCAAACTCTCACTGTGAATGGACCATTCAGTCTAAACTCTGGGTTTGTCTATCCCACTAA
 GATTGTGCATGTTGAGTCTGGAGTTTCACTACATGTGCCAGTATGACTATGTTGAGGTTCTGTATGGAGCAAC
 CGCGATGGCCAGATCATCAGCGGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACT
 CCACGTCCTCTTCCACTCCGATGGCTGCAAGAATTTTGACGCTTTCCATGCCATTTATGAGGAGATCAGCAGAT
 GCTCCTCATCCCCTTGTTCATGACGGCAGCTGCGCTCCTTGACAAGGCTGGATCTTACAAGTGTGCCCTGCTTG
 GCAGGCTATACTGGGCAGCGCTGTGAAAATCTCCTTGAGAAAGAACTGCTCAGACCCCTGGGGGCCCTGCTCAA
 TGGGTACCGAAAAATAACAGGGGGGCCCTGGGCTTATCAAGCGGACGCCATGCTAAAAATTTGGCACCCCTGGT
 TCTTTTGAACAACTCCTATGTTTCTAGTGGCAATGAGAAAAAGAACTTGCAGCGAATGGAGAGTGGTCAAGG
 AAACAGCCCATCTGCATAAAAGCCTCCCGAGAACCAAGATTTTCAAGCCTGGTGGAGAGGAGATTTCTCCGAT
 GCAGGTTGAGTCAAGGGAGACCCATTACACAGCTATACTCAGCGGCCCTTCAGCAAGCAGAACTGCGAGATG
 CCCCTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAG
 TATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGTGAGGACTGGGAAGTGGAG
 TGGGCGGGCACCATCCTGCATCCCTATCTGCGGGAAAAATTGAGAACATCACTGTCCAAAGACCAAGGGTGTG
 GCTGGCCGTGGCAGGAGCCATCTACAGGAGGACAGCGGGGTGCATGACGGCAGCCATACACAGGGGAGCGTGG
 TTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCAGCTGTGGTGGTGGCTGCCCATCTGTGTACTGACCTGGG
 GAAGGTCACCATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTACCGGGATGATGACCGGGATG
 AGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCATCCCACTATGACCCCATCTCTGCTGTGATGT
 GACATGCCATCCTGAAGCTTCTAGACAAGGCCGATCAGCACCCAGTCCAGCCCATCTGCCCTGCTGCCAG
 TCGGGATCTCAGCACTTCTTCCAGGAGTCCACATCACTGTGGCTGGCTGGAAATGTCCTGGCAGACGTGAGGA
 GCCCTGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCACTGTGGTGGATCTCGCTGCTGTGTGAGGAGCAG
 CATGAGGACCATGGCATCCAGTGAAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCCCTTC
 TGATATCTGCATCTGACAGACAGGAGGCATCGCGCTGTGTCTTCCCGGAGCAGCATCTCCTGAGCCAGCT
 GGCATCTGATGGGATCTGTGAGTGTGAGCTATGATAAAACCTGAGCCACAGGCTCTCCACTGCCTTCAACAG
 CTGCTGCGCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAGTGTTC
 TGTATATCCGCTCTGACTGTGTCTTGGTGAAGCAGTGTGGGCCCTGAAGTGTGATTGGCTGTGAACTTGG
 CTGTGCGGCGCTTGTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAAGTGAAGCTTCAATGGTGGTGAAGCTGAT
 GCCCGCCCACTACIAGACAGCAAACTGGAAGATGCCAGGCTTGAAGAACTGAAGTTTCTTCAAGAGAAC
 ATATACAAAACCTCTCCACTCCACTGACCTGGTGGCTTCCCAACTTTCAAGTTATAGATGCCATCGCATCTG
 ACAGGGAAGATCTGGGCTTCATGAGGCCCTTTGAGGCTCTCAAGTCTTAGAGAGTGCCTGTGGGAGCAGC
 CAGGGCAGCAGAGCTGGGATGTGGTCAAGCTTTGTGATAGGCCACAGTACAGTCTGTGCTTTTCCTTCC
 CCATCTCTTTGACACATTTTAAATAAATTAAGGCTTGGCTTCTGAAGTACAAAAAATAAAAAAAAAAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENINIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAACHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTS FQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCAAGTTCGCAATCAGATTGGAAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCTTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTGGGTGGGCCACCAGTAACACTTCGTGGGTGCCATTCAAGAGATTCTTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCTCATTTTGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAATTGACAACCTGTCCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGGTA AAAAGT
 TTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATGGGAC
 TGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACCTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAG
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCCAGAGTCTGG
 AGAACAGATGGGTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTTCTGGTTGGTGCA**TGA**CCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGTATTCTTTGTTTGCAATAATTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTTACAGCTCATTGTTGAGCTGAATTTTCTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGCGCTCCACAAAAGAGGGGAGAAAAGGCAGCAATCA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGAGGGTGGAGTGTGCGCTGCAAAAGGCAG
 CAGTAGCTGAGCTGGTGTGAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAAATA
 TGCTATCAAATACCTCTGTAGTAAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLTFFHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKÇEEHPKHLVVGRNSTGYRLYSGYFGGVLTALSREQFFKVNG
FSNNYWGWGGEDDDLRRLRVELQRMKISRPLPEVGKYTEMFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

CGTGGGCCCGGGGTTCGCGCAGCGGGGCTGTGGGGCGCCCGGAGGAGCGACCGCCGAGTTCTC
GAGCTCCAGCTGCATTTCCCTTCGCGCTCGCGCCACGCTTCTCCCGCTCGGGCGCCCGGCAATG
GCCAGGAGCTGTGGTTCGCGCTCGCGCCAGCTCTCTGGCTTGGCTGCCCTCTCGGCTGGG
CCCCGACGGGTGGCCCGCAGGCCTGTATGAACCTAATCTCACCACCGATAGCCCTGCCACCA
CGGAGCGGCTGGTGACCATCTCGGCCAGCCTGGTGGCCAAAGCAACGGCAGCCTGGCCCTG
CCCGCTACGCCCACTCTTACCCTCTCCACTCTCCAGTCCACCCGCTGGTGCTTACTGGCAA
GATGGAGAAAGGTTCTAGCTCCACCATCGGTGTGGTCGGCCACGTGGCCGGGAAATTCCCG
TCTGTGTCTGGGTCTACTGCGCTGACTGCTGGATGTCCAGCTGTGGCCAGGGCTTGGG
GTCTCTCCCATCAGAGATTCTCTGTGGGGGACCTTGTGTGTCACCAGAACACTTCCCTAC
CTGCGCCCAAGCTCTATCTCAGTAAGCCCTCTGGAAGTCTCTTCTCTCCCTCCACAGCCCA
GCAACTTCTCAAGACCGCTTGTTTCTCTACAGCTGGGACCTCGGGAGCGGGACCGAGATG
GTGACTGAAGACTCCGGTGTCTATTATAACTTTCATCATCGGACGCTTCAACGTGAAGCT
CAAAAGTGGTGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACAGGGCTGTGAAGCAAGA
CCGGGACCTTCTCCGCTCGTGAAGCTCAGAAACCCCTCGAGGCATCCAAGTGTGGGG
CCCCCTTAATCAGACCTTCCAAGAGTACCGGTGACCTTGAACCTTCTGGGGAGCCCTCC
TGTGACTGTGCTGGGCTCTCAAGCTGAGTGCTGCCATGATGTGCTGGAGGAAGGGGATGCCAC
CTGTGTCCGTGGCCAGCACGCTTACAACCTGACCCACACCTTCAGGGACCTTGGGGACTAC
TGCTTTCAGCATCGGGCGCGAGATATCATCAGCAACACATCAGTACCAAGATCCAGGT
GTGGCCCTCCAGAACTCAGCGCGGCTGCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA
TGTGTGGCTTTCATCATGTACATGACCCCTGCGGAATGCCATCGACAAAAGGACATGTTGGGAG
AACC CGGAGCCACCTCTGGGCTCAGGTGCTGCTGCCAGATGTGCTGTGGGCTTCTTGTCT
GGAGACTTCATCTGAGTACCTGGAATTGTTCGTGAGAACACCGGCTGCTCCCGGCCCTT
ATAAGTCTGCTAAAACTTACCCCTCTGCAAGCACTCCCCACCCCATCTCAGTGTAA
CTGACTGCTGACTTGGAGTTTCCAGAGGGTGGTGTGCACCATGACCAAGAGGGGTTCAAT
TGGCTGGGGCTGTGGGCTGGATCATCCATCTCATGTACAGTTCGACCATGCCACAAGCC
CTCCTCTCTGTCAACCCTGACCACGCCATCACCACCTGTACAGTCAGCCACTGACA
TAAGCCCATCTCGTGTACCACCCCTTGACCCCTTACCTTTGAAGAGGCTTCGTGCAAGGACT
TGTATGCTTGGGGTTCCTCGGTGTGACTCTAGTGGGCTGGCTGCCCATGCCATGCCCTCT
CTCATATTGGCAGTACTGCTGTCATTTGGGGGTTCTCAGTTTCTCCCTCCAGACAGCCCTAC
CTGTGCCAGAGAGCTAGAAGAAGGTCATAAAGGTTAAAAATCCATAACTTAAAGGTTGATC
ACATAGATGGGCACACTCAGACAGAGAAGTGTGCATGTACACACACACACACACACAC
CACACACACACAGAAATATAAACACTCGCTGCATGGGCATTTCAGATGATCAGCTCTGTA
TCTGGTTAAGTGGTGTCTGGATGACCCCTGCATAGAGCTGAAAGGAAATTTGACCTCA
AGCAGCCCTGACAGGTTCTGGGGCCGGGCCCTCCCTTTGTGCTTTGTCTTCGATTTCTTG
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGACAGGGGCTGGATGGGGGCGAGACT
AATACTGAGTGATTGCAAGTGCTTTATAAATACACCTTATTTTACGAAACCATCTGTG
AAACTTTCACTGAGGAAGAGCCCTTGACCGGTAGAAGAGGTTGAGTCAAGGCGGGCGCGG
TGCTCAGCCCTGTATATCCAGCACTTTGGAGGCGCGGAGCGGGTGGATCAGAGATCAGGA
GATCGAGACCACTGGCTACCAACCGTGAACCCCGCTCTACTAAAAAATAAAAAAGTT
AGCCGGGCGTGGTGGTGGGTGCTGTAGTCCAGCTACTCGGAGGCTGAGGCAGGAGATG
GTGCGAACCCGGGAGGCGGAGCTTCAGTGAAGCCAGTGGCGCCACTGCATCCAGCTGA
GTGACAGCGCAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWSSYLTKTVLKVSFLLHDPNSNFLKTALFLYSWDFGDTQ
MVTEDSVVYYNYSIIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCMCCGPFLLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTCCCA
CAACAGACGGGACAACTTGCAAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCATCTGCATTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCCGTCCCTCCCTTCCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGAATAAAA
TGGCTGGTTCTTTTGTTCCTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

0903521-11401

165/330

FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

0902521-11403

FIGURE 166

CTGT CAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTCTCTGTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTCCACCTCCTTCTCGTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAGCCCTACACCAC
 GGAATCATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAAGT
 GAGTCTTGGAACTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTCTGGGGGTTAGGAGTGCTGATTCCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTCGCTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACCGGGGACTCATGGGTGTGATTACAGAGAGCCATGGTGAAGCCCTG
 CCCACACGCTCTGGTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC
 TGTGCTATCAAGTATGACCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGCG
 CATTTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACCAC
 AAGGACAGGAGCCGCTCT**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCACTGCTGTGCTTCTCCAGACTCCAGGG
 CTCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGTGCCTTGTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGCCTGACAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGCGGCCACCCG
 CTCTCAGGAAAGGCACAGCTGAGGCATGTGGCTGGCTTCGGCTCAACATCGCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCTATGTCAGGGGCTTTGAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTGCTACTCCAGGCTAACCTGAACTCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTGAATTCCTACCTCACAGGGCTGTTGTGGGGATTAAAGTCTGCGGGTGAATGA
 AGGACACATCACGTTCAAGTACAGGCCCAAAACGGGGACGGCAGGCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTTCTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVIIVPAIFGVSEFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRGSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAAELESWNLLSRTNYNFYQYISLRLTVLWGLGVLI RYCFLPLRIALFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH
TSPIDVIIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

FIGURE 168

G C C C C T C G A A A C C A G G A C T C C A G C A C C T C T G G T C C C G C C C T C A C C C G A C C C C T G G C C C T C A
 C G T C T C C T C C A G G G A T G G C G C T G G C G G C T T T G A T G A T C G C C C T C G G C A G C C T C G G C C T C C A C
 A C C T G G C A G G C C C A G G C T G T T C C A C C A T C C T G C C C C T G G G C C T G G C T C C A G A C A C C T T T G A
 C G A T A C C T A T G T G G G T T G T G C A G A G G A G A T G G A G G A G A A G G C A G C C C C C C T G C T A A A G G A G G
 A A A T G G C C C A C C A T G C C C T G C T G C G G G A A T C C T G G G A G G C A G C C C A G G A G A C C T G G G A G G A C
 A A G C G T C G A G G G C T T A C C T T G C C C C C T G G C T T C A A A G C C C A G A A T G G A A T A G C C A T T A T G G T
 C T A C A C C A A C T C A T C G A A C A C C T T G T A C T G G G A G T T G A A T C A G G C C G T G C G G A C G G G C G G A G
 G C T C C C G G G A G C T C T A C A T G A G G C A C T T T C C C T T C A A G G C C C T G C A T T T C T A C C T G A T C C G G
 G C C C T G C A G C T G C T G C G A G G C A G T G G G G G C T G C A G C A G G G A C C T G G G G A G G T G G T G T T C C G
 A G G T G T G G G C A G C C T T C G C T T T G A A C C C A A G A G G C T G G G G G A C T C T G T C C G C T T G G G C C A G T
 T T G C C T C C A G C T C C C T G G A T A A G G C A G T G C C C C A C A G A T T G G G G A G A A G A G G C G G G G C T G T
 G T G T C T G C G C C A G G G T G C A G C T A G G G T C A C A A T C T G A G G G G G C C T C C T C T G C C C C C C T G
 G A A G A C T C T G C T C T T G G C C C C T G G A G A G T T C C A G C T C T A G G G G T T G G G C C C T G A A A G T C C A
 A C A T C T G C C A C T T A G G A G C C C T G G G A A C G G G T G A C C T T C A T A T G A C G A A G A G G C A C C T C C A G
 C A G C C T T G A G A A G C A A G A A C A T G G T T C C G G A C C C A G C C C T A G C A G C C T T C C C C A A C C A G G
 A T G T T G G C C T G G G G A G G C C A C A G C A G G G C T G A G G G A A C T C T G C T A T G T G A T G G G G A C T T C C T
 G G G A C A A G C A A G G A A G T A C T G A G G C A G C C A C T T G A T T G A A C G G T G T T G C A A T G T G G A G A C A
 T G G A G T T T A T T G A G G T A G C T A C G T G A T T A A A T G G T A T T G C A G T G T G G A

FIGURE 170

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGCTCTGGACCTTCAACACAACCCCTCTTGTCCACATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAAATGAGTC
CCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTGTGGTGCCCT
CCTGCTCAGTCTCTTTGTAAGTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCAT
TCTGGAGAGAAACACAGGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGAAAAATCCCCACTCAC
TGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCTAAGTCTCTGCTCA

0902521 111401

MAGSPTCLTLIYLWLQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYVVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVMTGLQSNKNGTCVTNL7CCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNFVSRNFSSPILARKLCEGAADPDSSMVLCLLLVPLLLSLFVLGLFLW
FLKRERQEYIEEKRRVDICRETPNICPHSGENETDYDTPHTNRTILKEDPANTVYSTVEIP
KMNPHSLLTMPDTPLRFAYENVI

FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCCTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAAATGGGTCCATCTCCCATCTCTCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTGAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCT
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGTGGACATTTGTCGGGAA
ACTCCTAACATATGCCCCCATCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATAACCGAAAA
AGATGGAATAATCCCACTCACTGCTCAGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTGAGTTCAGACATCAAGGAAA
GGTTTGCAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAAT
TTTTCATGAAATTATTCCTCTTCCCTGTTCAATAAATGATTACCCTTGCACTTAA

0993521.1.1401

FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHG NFRLFLEQ
IHVLENSLV LKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

090251-11401
10477-1252660

GGCTTCGACGCTTTCTGAGCCAGGGGTGAC**CATG**ACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTACAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAACATAGGCTTATCCAGTTCTCAGTATTTTTAGGTCTATTGCT
TGTGTTGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTACATCGGTTTCTTGCGCTGT
TGTGTGGAGTCTTAAGCGAAGAAGTCAAATTGTG**TAG**TTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAA

Journal of Management Inquiry 22(1) 3-17

Journal of Management Inquiry 22(1) 3-17

Journal of Management Inquiry 22(1) 3-17

FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAAATAGTGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

00051.11401

178/330

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKRRLSLKKSWWK

000000.111101

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

180/330

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCK
YKSSQKQHSPVPEKAIP LITPGSATTC

099551.11401
10444.122260

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
TGGCTGGGCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCC
AGTGTTCCTCCACAGCCCCCAAACGGAAGTGGTTTTGGGGTCACCTGGGCTGATCACTCCT
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGT
ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGTAAGCCCTGG
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
GCCCGCTTCCATTTCACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAAACA
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACGCTTTTGAG
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGACATCTTCAGCTTTCAGACGCTATTG
TCAGGAGAGGGCCAGTGAATATATTGGCCACCATTTCGAGCTTCAGTGCCCTTGTAGAGAAAA
GAAGCCAGCATATCCTCCAGCACAATGAGACTTTCGTATTACCTCTCCCATGACGGGCGGCGC
TCCACAGGGGCTGCCGCTGGTGCACTGACTTCACAGACGCTGTCTATCCGGGAGCGGCGTCG
CACCTCTCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT
ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCAGGCCAGTGGCCTCTC
CTGGGTCTGTACAACCTTGCAGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
AAGAGCTTCTGAAGACCGCGATCTTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCC
TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
TCATCGATATTATAGGGGTCCATCACAACCCAACCTGTGTGGCCGGATCCTGAGGCTACGAC
CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATCTTCTCTC
CGCAGGGCCAGGAAGTGCATCGGGCAGCGCTTCCCATGCGGAGATTAAAGTGGTCTCTGG
CTGTGATGCTGCTGCCATCTCCGTTACCTGCGAGACACACTGAGCCCCGAGGAAGCTGGAA
TGATCATGCGCGCCAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGAATGTAGGCTTGCA
GTGACTTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSI TNASAAIAPKDNLF
IRFLKFWLGE GILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMEFHISLMTLDSLQKCIFSFD SHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTD AVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLLSKDE DG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTTAACCCAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCTGATTGCTTCTGGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAC
AGTGTGGAGAAAAACTAGGCCAAACTACACCTGTTTCATTGTTACCTGGAAAAATAATCCTCT
ATGTTTTCACAAAAA

FIGURE 185

GAACATTTTGTAGTTCCTCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACCTGTA

186/330

FIGURE 186

MPSPGTVCSELLLGLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

099554-11404

CGGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCTCTGCTGTATGTCCTCGTCCAGTACCTC
GTGAACCCCGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAAACAGTGGTGCTGT
TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
CTCTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGTGCTCATCTTCCACATCTACCT
GAGTATGTCCCCACCTAAGCCCCCGATCCCCCAAGGCTGGTGGTCAGAGCTGCTCATC
TTACACCTCTACTTGAGTATGTCCTTAACCTGAGCCCCCAGCCTGGGGCCAGAGTCTTT
GTCCCCGTGTGCGCATGTGTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAAA
GGGCAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAGAAGAGCTGAAC
TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTACA
GACAAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
CCAAAAACACAAGTAGAAATTCTAACAAATGAAATATATTACAGGCAGGTCACCCACTAACCA
AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
AGTCATGTTGCTGAACGACGAGGGGTAAACTCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
AACAAACAACCTCCCTGCTCTGGCACCAGCCGTTTGGTTCATGGTGGGCCAGCTGCAAAGCG
TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
ACGGGCAGCAGAGTGTGTCCAGGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAAATGAACACACCCACCAAGA
GCCTCCTTGTTTATAACACAGAGTTACCCTACAACCACTGTCCCCACACACCTCTGGGGAT
GTTTTTAAACACACACCTCTAAGTCATATCTTACAGTCACTGTTGTCTTGCTTGAGGGTTGA
ATTTTTTTTTAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

188/330

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLS PRSPQGW
VVRAAHLTPLLEYVPNEPPTPGARVVFVRVRCSGSASPRSEIMDKKGSQEEIKSMRTQQ
AQQEAEELTPRPAGVVPGA

090254-11401

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGCACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAAGTGTCTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCGCGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGTTATCCCTGGGAACGAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCCTCTGTCTGTCTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATATGGGCTG
 GGCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTGGCTGTCAACACCTTCA
 ACAGTACACCAGGATGGTGTGGAGTTCAAGTGCAAGCA**TAG**TAAAGAGCTTCAAGGAAAC
 CCGAAGTGCCTACCACATCACCATCAGTGTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGGTTTGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTCGGGTGCCACTGCTCTCTTTTCCCTCTACAGCTCCATCTTGTTTACCCAC
 CCCACATCTCACACATCCAGAATCCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTGGGG
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNTSTQEVVQYNWETGDDRFSEFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRIMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFVTSLSDCQLGSRRLTTTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVVHVDGAGVQVQA

000221.11401

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTTGGTTACCCCTTGGTCTCCTG
 TCTTTATGTCTTTCTCCTCTTCTCTATTCTGTCACTCTCCCTCACTTAAGTCTCAGGCCTGTCA
 GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
 TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
 GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
 AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCTCTCCCAA
 GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
 CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
 AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTGAG
 GACATTGCCCTCTGTGTGCCACCAACCAGGACTTCCCCCTTGGCTTGGCATCCCTGGCTCT
 CTCCTGGTACCCAGCAAGACGTCTGTTCAGGGCAGTGTAGCATCTTTCAAGCTCCGTACT
 ATGGCGATGGCCATGATGTTACAATCCCCTTGCCTGAATAATCAAGTGGGAAGGGGAAGCA
 GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAA
 GGAAGCAACAGGAACTTCTGCAACTGGTTTTATCGGAAAGATCATCTTGCCTGCAGATGC
 GTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
 ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG
 AAGTCACTCAGCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
 AACCAAGGAACTAACAAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
 CATGCCACCAAAACAATAAAACAAATTTCTCTAACTGAAA

090221.1141
 191/330

192/330

FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQLACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGSME
HRNHLCFCDLYDRATSPPLKCSLL

0992521.11401

FIGURE 193

GTAGCGCGCTCTTGGGTCTCCCGGCTGCCGTGCTGCCGCCGCCGCTCGGGTCTGTGGAGCAGGAGCGACGTCA
 CCGCCATGGCAGGCAATCAAAAGCTTTGATTAGTTTGTCTCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTT
 GGTATGTGCCCTTCCAATATACAACAAATACTGGCCCTCTTTGTTCTATTTTTTTACATCCTTCACTATTTCC
 ATACTGCAATAGCAAGAAAGATTAGTGGATGATACAGATGCTATGAGTACGCTTGTGAAGGAACCTTGACATCTTTC
 TTACAACGGGCATTGTCTGTGTCAGCTTTTGGACTCCCTATTGTATTGTCCAGAGGCACATCTGATTGAGTGGGGA
 GCTTTGTGCACTTTGTTCTCAGAGAAACACAGTCATCTTTGCCAATATACTAGGCTTTTCTTGGCTTTTGGAAAG
 CAATGACGACTTCAGCTGGCAGGAGTGGTGAAGAAATTTACTGAACATTTGTCAAAATGGACTTCCTGTGATTT
 GTTGGCCATTCCAGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAAGCATACTATTTTCCAGAGAGCTTGCTGAAGGATTAAAGGATTTTCT
 CTTTGGAAAAGCTTGACTGATTTACACCTTATCTATAGTATGCTTTTGTGGTGCTCTGCTGAATTTAAATAT
 TTATGTGTTTTTCTGTAGGTTGATTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAAATGTAATCA
 TTTGCAATTGGTTAGGAATTTCAGAAATCCGCCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATATTT
 TAGCTCCATTATTACAAAAAATTATAAAAAAAGTTTTCACTAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAGTGTTAATGCCATGCCCTCCGTTAAGGGTTTGTGGTTTTACTGGTAGACAGATGTTTGTGGATTG
 AAAATTAATTTATGGAATTGCTACAGAGGAGTGCTTTTCTCAATTTGTTAGAAGAATTTATGTTAACTTTA
 AGGTAAGGGTGTAAAAACATTTTGAGATAAGGTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGT
 GGGAGAAGATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTATAAGTGAATTTGTGATCTCCTATC
 AACCTTTCATGTTTTTACCCTGTAAAAATGGACATACATGGAACCACTACTGATAGGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAACCTTCCTCTGCTTCTCCTTTTGACTTATTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAATATAGTTTAATAACCTTAGAAGTGTACTTACTGGAAAAATTTGCTATGCCGTACATTT
 CAGAGTGCCCTCCCTCGAAGGCCCTGGCATGATTAACAGTAACCTGTTAGTCTTACAGATAATTCATGCA
 TTAAACAGTTTAAAGATTAGACATGTTAATAGTAGTTCATTATTCTTAAGGTTATATCATATGTAAATTTAAAG
 TATTTTAAAGACAGTTTCTGTTATACCTCTGAACCTGTTTGAATTTGAGTTCATCATATAGATCTGCTGTTGT
 CCTTTAAAGGCAATTTGTTGTGTAGTTAATGCAAGTAGCCAAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATCCCGATAACCAAGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTTATCAGGA
 CTTTATTTCAGGAGTGGGTTATAAAAAACATTCAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTGTATG
 TTTATTCACTATACCTACATAAAAAATTTTCGCCATAGCCAAACCTCAGTAATCATGACAGCTGCTCTGTTGT
 TTTATGAAGTTTATTTCTCAAGAAAAATGGGAATAAATTTGGGAATTTGTCACTTTTTTACTAAAGATGCCATA
 AGCCACAGGTTTTATTGCCATACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG
 GCGTGTGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGGCTTGTGATTATAATGTTCAAGATTTCAAGAGGAA
 GGTGCAAGTACAAATGAGTTAGAGAGCTGGTGACAGAGTGGGAACCTTTTGTGCTGTGATCTACTGGAATTT
 TTTTTCAGGAAGATGCATTTCTGTGCTCTCCCTATTTTCTGTTCTGGATGTCAAGTCAAGTCACTGCTACTG
 TTTTATCCACTTGGCCAGACATTTTCTAACAGCTGGCTATTTTCTATATACAAATGCAATGGCAGCAT
 GTGCTTTGAGATGTATACCTAGCTTGACATAGTGTCTGTCTGATTTCTAGGCTACTTACTTGAATATGAAT
 TTTTCAATAGCAATGCACTGTATACACATTTACCATCTTCTATGAAAGAAACCTTTTGATGATGAACATATA
 AGATTTTAAATCTATTTTAAAAAATAA

MDFFLLGLCLCYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQOFTGLMQLTWLYLDHNHICSVQGDAPQLRRVKELTSSNQ
ITQLPNTTFRPMENLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQVFPVRIQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNFAHFPRILISLHSLCLRKNKVAIV
VSSLDVWVNLEKMDLSGNEIEYMEPHVFTETVPHLQSLQLDSNRILTYIEPRILNSWKSLSIT
LAGNLWDCCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGAEPTSG
HLLSAVNTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVYVSWKCFPSLRQLQRCFVTQRRKQKQKQTMHQMAMSAQEYVVDYKPNH
IEGALVINEYSGCTCHOOARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCTCTGGGCCGGGTCTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCAGGACCCCGTGCGCCGGCGGCCGCTTGAGTTCGCCGGCGACAAGATGG
TGTCAGTCTCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCTTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCTGCCCTGCCGC
CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTTCCGCTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTTGGCGTCCCGCGGGCCGCTACGCTTCCACGGGCCGGCGCGCTTGAGCCTG
GGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

09951-1101

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLPLDGLVLASGAGFVSDVSGSHLDCGAGEPAVFRSDRFSWHDPLWRSNGDEA
PGLFFVDAERVPCRHHDDVFPPSASFRVGLGPGASPVVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPGLSVGPEDCADPSGCVCGNAEAQPWICALLQP

[illegible]

TTGAGCGCAGGTGAGCTCTGCGCGTTTCGGGGGGCGTTCTCCAGTACCCTCCGCGGTTACCGCGCGCGCGC
CGAGGAGGAGCTCTCTCCAGACCGCTCCCTCCGGTTGCTCCAAACTAATCGGAGTGAAGCGATCGCTCGAGGAGT
GGGAGAGAAATTTAGGGGGGAGAAAGGACGAGAGACACATACCATCGATCCGAGATAGATTATTCTTACACTG
AAGTCATCAAGTCAATTTGAAATAGCATCTGCAAATTTATCTTGGTGCTCTCATACTTGCCTGCATGACTTCTT
AACCCCTTTTCTCTCCAATAGCAGCAGAAAGGTTCTACTAGTTTCTTTGTAGTATCCGTTGGGATTTCT
TATATAAGTTTCCAAGCGCCCATTTTCTATTATATATGATAAATATGGTGTTCACGTGAAGCAAGTTACTAATGT
TTTATTACAAAACCTCCTCAACATTATATCTTGGTAACTGGCCCTCTTTCAGAGAACTATGGGATTTGTGT
AAATGAATGTTTGTATCCTATTCCGGAACAAATCTTCTCCTTGATACATGAATTTATGTATGTTCCAAAGTTT
GGGAAAGAACGACCAATATGGATCGACAACCGAGGGCGAGCACATAGTGGTGAGCCATGTTGGCCCGGA
ACAGATGTAAATATCATATAGCGCTTTCTCTACTCATATACGCTTCAACATGAGTCAGGTTTCATTGGAAGATGAG
AGTTGCCAAATTTTGAATAGTTTACGTCAAAGAGGCCATAAATCTTGGTCTCTCTATTTGGGAAGCCCTG
ATGACATGGCCCACTTTGGGACCTGACGTCCGCTCATGGGCGCTGTCAITTCAGATATTTGACAAGAGTTA
GSAATCTCTATCAACAAATCTGTAAAAGGCAAGTTTGTGGAACATCTGCAACTAATCATCAAGTGATCATGG
AATGACGCGACTGTCTCGAGGAAGGTTAATAGAATCTGACCATCTCGGATGAAGAACCATTAACCTTGATTG
ATCAATCTCCAGTAGCAGCTCTCTGCCAAAGAGGTAAGTTTGTGAGTCTATGAAGCACTAATCAAGCT
CATCTTAATCTTACTGTTTACAAAGAAAGACAGCTTCAGAAAGTGGCATTAACAAACAACAGTCGAATTCA
ACCAATCATAGCAGTGGCTGAGGAAGGTGGCACTTTTACAGAAATGAGTCAGATGACTTTCTGTAGGCCAC
ACGGTAGCATAAATGCGTTAGCAGATATGCATCAACATTTTGGCCACTGGTCTGCCCTTCCGAAAGAAATTC
TCAAAAGAGCCGATGAACTCCACAGATTGTAGCACTACTATGCGACCTCTCATATCTCGCATCGCCACA
CATGATGATCATCTGGAATGTCAGAGTCTGCTCAATTCAGCAATGCGAGGGTGATGCGCTTATACACAGAGTA
CTATATCTCTCCGCTGGTAGTGTAAACAGCAGCAATATGACCAAGGGGTCACTCCCTATTATTCATGGGGT
TCTCTTGGCAGATATATAGTATGTATTTTGTATTTTCTTATTAAGCATTTAATTCAGATCAATATCCGCT
CTTCAAGATATGCTATCGAATAGCTCAACCATTTATCAAGCGCTAAGTACTTGAAGTGGATTCGATAT
TTGAAGTGGAGATTCCATAATATGTCTAGTGTTTAAAGGTTTCAAATCTGGGAAACCGAGTTCACAACTCTCC
AGAAACCATTAAGACGTTACATATTTAGGTATACACACACACACACACACACACACACACACACACACAC
ATACTTACACCTGCAAGGAATAAAGATGTAGAGATGTCTCATTTGCTATGACATGGGATAGGATAGA
ATCTGCTCTTTATTTGGACTTGGCGAGATATGTATATATTTAGCAACTTTCGACATGTGAAGTACTTATAT
ATTGCCTTTAAATTTCTCTCTGTGGGTGACTTTAATTTGAATGCACTTTATGACAGTTATGCTCTTAAC
TTAGTTGAAATGACAACTTTTTCGACCAATGTCACAGATATCTGTTACGCTATGTTCCAAATGAAGAAAT
TCTAATAATCCGGAATATGAACATAGAAATCTATCTCATATAATGAGAGAGAAGAGGTTGATAAGTTGTA
AAATTAATGATGATAACCTTTGAACCTTGAATTTGGAGATGATTTCCCAACAGCAGATGCACTCTGGGCACT
TCTGTGCTTATTTCTTTCAGAGACGTGGTTTCTTATTATTTCTCCCAAAGAGAGTCAATACTGACGAG
ATTCTGTTCTAATATATGTTCTGTGCTATAAAATATTGTGATTTCCCTGATGAGTCATATCTGATGATTTCA
TAAATATGAAGACCATTAATATACTTTCTTCTATATGTCAGCATGGCTGAATAGAGAACACGGCA
CCATCTCGACATGTTGTTCTCTGTGTTGAATATTGCTCTCTTGAATAATTAATCACTATTAATACATTAA
AAATCAAATTTGGATAAAAAATAAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVLSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEATPIW
ITNQRAHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGFPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDHYYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

GGATTTTTGTGATCCGGATTTCGCTCCCACGGCGGGGACCTTTGTAAC TCGGGAGGCCCAAG
GACAGGCCCAACCTTGC GGCGGGGAGGCAGCCGGGTGAGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCCCTTGCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGA ACTCACAA
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTACCCGCGAGGGCC
AAGGTGGCTCCGCTGAGAGGATGAGCAAGTTCTTAAGGCATCTACGGTCGTGGGAGACGA
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
AGCAGCCACCACCACACCACTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCC
CCTGCCCTGGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
CAGCTCCACAGGTTTACAGTTCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCGACAGAATAACTATGTCGCATG
GTATTCACCTACATGAGCATCACCATCTTGGTCTTTTTATGATGGAGATCATCTTTAAAT
ATTTGCTCTCCGCTGAGTCTTTTACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTG
TGGTCTCATTATCCTGGACATTGTCTCTGTTCCAGGAGCACCAAGTTTGAGGCTCTGGGC
CTGCTGATTCTGCTCCGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTGAGAACGGCAACTCTTAAGGTAAAAACAGATGAATGTACAATTGGCCGCCA
AGATTCAACACCTTGAGTTCACTGCTCTGAGAAGCCCTGGACTGATGAGTTTGCTGTATC
AACCTGTAAGGAGAAGCTCTCTCCGATGGCTATGGGAATGAAAGAAATCCGACTTCTACTCT
CACACAGCCACCCTGAAAGTCCTGGAGTAAATGTGCTGTACAGAGAGAGAGAAGGAAG
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACGAGAACCTGACAGTCACTGGCCAGTTA
TCATTCAGATTACAAATCACACAGGATCTGCCTGTTTTCATCACAAGAGAACAACCA
AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MATWDEKAVTRRAKVAPAERMKFLRHFTVVGDDYHAWNINYKKWENEEEEEEQPPPTFV
SGEGRAAAAPDVAPAPGAPAPRAPLDFRGMRLKLFSSHRFQV I I C L V V L D A L L V L A E L I L D L
K I I Q P D K N N Y A A M V F H Y M S I T I L V F F M M E I I F K L F V F R L S S F T T S L R S W M P V V V V S F I L D I
V L L F Q E H Q F E A L G L L I L L R L R V A R I I N G I I I S V K T R S E R Q L L R L K M N V Q L A A K I Q H L E F S
C S E K P L D

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCCGCCAACAT
 GCTCTGTCTGTGCTCTACGCTGCCGGTTCATCGGGGAAGGCCAGACCGAGTTCAGATCTTTG
 AGTCCGAAGGGGCTCCCTGCGGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCTCATCCCTCC
 CAGGAACTTCCAGCTACCCGCCAGTGGAAAGCAGAAAATTGTACAGCTGGAGATAGGACCTT
 TGATGGGCGACTAGACTTTGAAGAATTTGTCCATTATCTCCAAGCTCATGAGAAGAAGCTGA
 GGCTGGTGTAAAGATTTTGGACAAAAGAATGATGGACGCTTGACGCGCAGGAGATCATG
 CAGTCCCTGCGGGGACTGGGAGTCAAGATATCTGAACAGCAGGCGAGAAAATTTCTCAAGAG
 CATGGATAAAAAGGGGACATGACCATCGACTGGAACAGAGTGGAGAGACTACCACCTCCCTCC
 ACCCGTGGAAAAACATCCCCGAGATCATCTCTACTGGAAGCATTCACGATCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGG
 ACAGGCTCAAGGTGATTCGAGAAGGAGGGGCCAGTCACTCTGGCGGGGCAATGGCATCAA
 GGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGTCACTCTGGCGGGGCAATGGCATCAA
 TGCTCTCAAAATTTGCCCGGATACAGCATCAAAATTCATGGCCTATGAGCAGATCAAGCGCC
 TTGTTGGTATGTCAGGAGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCTTGGCA
 GGGGCCATCGCCAGGAGCATCTTACCAATGGAGTCTTGAAGACCCGGATGGCGCTTCGCG
 GAAGACGGCCGACTACTCAGGAATGCTGACTGCGCCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCGCGCTTCTACAAAGGCTATGTCCCCAACATGCTGGGCATCATCCCTATGCCCGGCATC
 GACCTTGCAGCTCTACAGAGAGCTCAAGAATGCTGGCTGCAGCATATCAGTGAACAGCGC
 GGACCGCGCGGTGTTTGGCTTCTTCCCTGGCTGTGGCACCATTGCCAGTACCTGTGGCCAGCTGG
 CCAGTCAACCCCTGGCTCTAGTACGAGCCGGATGAGGCCAGGCCCTTATTGAGGGCGCT
 CCGGAGGTGACATGAGCAGCTCTTCAAAATATCTTGGCAGCCGAGAGGGGCTCTCGGGCT
 GTACAGGGGCTGGCGCCCACTTCTATGAAGGTCACTCCAGCTGTGAGCATGAGTCACTGAGTGG
 TCTACGAGAACCTGAAGATCACCTGGGCGTGCAGTCCGCGTGAAGGGGGAGGGGCGCCCG
 GCAGTGGACTCGCTGATCTGGGCGCAGCTTGGGCTGTCAGCCATCTCATTTGTGAATG
 TGCCAAACCTAAGCTTCTCTGAGCCAAGCTGTGAAACCCCTAGACGCCACCCCGAGGAGGGT
 GGGGAGAGCTGGCAGGCCAGGCTTGTCTGCTGACCCAGCAGCCCTCTGTGGTTCCTC
 AGCGAAGCCAGAGGCAATTCCTTAGGCTCCAGGCTCAGCAGGCTCCGGGCTCATATGTATA
 GGACAGGACATTTTCTGAGTGCCTGCCAATAGTGAAGTGGAGCTGGAGGCCGGCTTAGT
 TCTTCCATTTACCTTTCAGCAGCAGCTGTTGGCCACGGCCCTGCCCTCTGGTCTGCCGTGC
 ATCTCCCTGTCCTCTGCTGCTGCTGCTGCTGAGGTAAGGTGGGAGGAGGGCTACAG
 CCCACATCCCACTCCCTCTGCTCAATCCCATATCCATGATGAAGGTGAGGTACGTTGGCCT
 CCCAGGCCCTGACTTCCCAACCTACAGCATGACGCCAATTTGGCTGTGAAGGAAGAGGAAAG
 GATCTGCTCTTGTGCTACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT
 TGGGAGTGCAGGGGGCTCGGGCTGCCCTGGCTGCGAGAGGCAAGTGGTGGGGCTCA
 TGCTGCTCTGAGCTGGCTTGGACCTGTGAGGATGGGCCCCACCTCAGAACCAAACTCACTG
 TCCCACTGTGGCATGAGGCGAGTGGAGCACTGTTTGAAGGCGAAGGGCAGAGCGTTTGT
 GTCTCTTGGGAGGGAAGGAAAGGTGTTGGAGGCTTAAATATGCACTGTGGGAAAAGGG
 TTTTGTCCAGAAGGACAAGCCGACAAATGAGGCACTTCTGTGCTTCCAGAGGAAGAGCAGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCTCTGGGGTTCCTGTCCAACC
 CCAGAGGGGCGCAGCGGAGGAGCCACATCCACTTGTGCTGCTGCTTGGAACTATTT
 ATTTTGTATTTTATTTGAACAGAGTTATGCTTAACATTTTATAGATTTGTTTAAATTAAT
 TCTGTGATCTTTCAAGTTCATTTTTATTATATTTATGTTATGTTGATTTGATTTGCTTCC
 AAGCCGCCCACTGGGATGGGAGGAGGAGGAGGAGGAGGGGGGCTTGGGCGCTGCAGTCACTG
 CTGTCCAGAGAAATTCCTTTTGGGACTGGAGGCGAGAAAGCGGCCAGAGGCAAGGACCCAT
 GCTCTCTTTCTTTGGCAGGTTGGGGAAGGGCTTGGCCCCAGCTTTAGGATTTCAAGGTTTGA
 CTGGGGGCTGGAGAGAGGAGGAGGACCTCAATAACCTTGAAGTGGAACTCAGGTTATTTG
 CTGCGCTGCAAGGCTTCTTTTATTTCACTCTTTTCTGAATGTCAAGGCAGTGAAGGTCCTCT
 CACTGTGAATTTGTTGGTGGGCGGGGCTGGAGGAGAGGTTGGGGGCTGGCTCGCTCCCTCC
 CAGCCTTCTGTGCTGCTTGTAAACATGCCGGCCAACCTGGCGACCTCAGGCTTGCATCTCC
 ATTTCCACAGGATACCTGATGAGGAAATCTCAATAGGATGCAAAAGATCAATGCAAAAAAT
 GTTATATATGAACATATACTGAGTCTGCTCAAAAGCAAATTAAGAAGAAGTTGGACGTTAG
 AAGTTGTCAATTTAAAGACGCTTCTAATAAAGTTGTTTCAAGCTGAAAAAAGAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKLK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRLKVLQVHASRSNNMGIVGGFTQMIREGGARSLWRNGI
 NVLKIAPESAIFMAYEQIKRLVGSQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTATCCAGATACGCTGGGAACCTTCCCCAGGCAT
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATATTATTCTGGCTGGAG
 CAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGGAGACACTCCATCAGTCACTACTGTC
 GCCTCAGCTGGGAACATTTGGGGAGGATGGAATCTGAGCTGCACTTTTGAACCTGCATCAA
 ACTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCC
 AAGAAGGCCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTC
 TGTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCACTCAGACATGTC
 GCGACCTCAAAATGTTATATCATCTCTTAAAGGCCAAGGGGAATGCTAACCTTGAGTATA
 AAATCGGAGCCTTTCAGATGCGCGAAGTGAAATGTGCATATAATGCCAGCTCAGAGACTTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCCAGGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATTCGGAGATCAAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTTCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAATGTGCCTTGGCCACAAAAAAG
 CTTGCACAAAGTCATTTGTACAACAGGGATCTACAGAACTATTTACCACAGCATATGACCTAG
 TATTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACACAGACA
 AGAACAACAAAGAGAACCCAAAGCAGAGGCTCCCAATATGAACAGAGTAAAFTCATCTTCAA
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTACAGCAAGTGTGTTAAGAGTGATAAG
 TAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT
 GGGGAGTGAGAGGACAGGATAGTGCAATGTTCTTTGTCTCTGAATTTTATGTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTTGAAAGTCTATCCCAACATATCCACATCTTATATTTCCA
 CAAATTAAGCTGTAGTATGTACCTTAAGAGCCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAAATTTTAGCATAA
 ACAGAGCAGCTGGGGACAGCAGTTTATAAAATAAATGAGCAGCTCTCTTTTAAACAAAAAA
 AAAAAA

FIGURE 208

MASLGQILFWSIIISIIIIILAGATAIIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

000001.11101

[illegible]

210/330

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAOQLLQEMKTLFLNTEYLMPFLL
LNQCGSLLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

0092521.11101

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCTCCCTTGGGAGAAGTCAGCTCCAGCACCAATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG
 AATCTAATGGAACTTCTGTGCTGGGAAGCCCTGGAATGCTATGAAGAAGAACAGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT
 CAACGTGAGTAACGCCACCTGTGAGTTCCTGTCTGGTGAAAAACAAGACTCTTGGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCCCACGCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAAGGTCTGGGGCTGCACTTTGCCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCTGCTCTGCCCCGTTTAAGTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA
 AAGCACTGGTTCATTCAGTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLET PVR
LYQNMFCSAENCSEETHITAFTHVHVSAAEHFHFVSQCCQGKCSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPKWCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTSHNVGSKASLYLLALASLLLRGLLP

212/330

FIGURE 213

GGGCTCGGTTCAAACGACCACCGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
GGGCTTGCCCTACTGGCCACCTCCCAACCCCAAGAGCCCAGCCCCATGTCCTCCCGCCGCG
GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGCGGGGGCCCAAGCGCTG
ACCCAGACTCCGACCGAAATGCGACGGGTCACTTTACGCTTTGGGGGCCCATGACCCGCGA
CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
ATGATGCCATGGCCGACGCGGACCGCTGGCTGGACAGCGCTGCCGAGCTCTTGCGCGCC
ACGGTGTCCACCGGCTTTAGCCGGTCGTCGCCATTAAACAGGAGGATGGGTCTTCAGAAGA
GGGGTTGTGATTAATGCCGGAAGGATAGCACAGCAGAGAGCTTCCAGTGCGACTCCCA
ATACAGCGGGGAGTTCCAGCAGCAGGTTTATAGCAATAGTCAGGAGCCTGAAATCAGGCTG
ACTTCAAGCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTACCCCTCACCCACAG
CCATGCCATCTCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCT
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC
CCTGCAACCAGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCACTGT
GCCTCTCAGAGCACCAACAGTACCAGGACCACCACTACCCCCCTCCCACCATCCACCTCAG
AAGCAGTCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
GGATTGGCTGGAGGATATTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
GACAGAAACCAGAGGTAAATGGCCACTTCATCCATCAGGAGATGTCAATCTCAACCTCT
CTGCCCTTTCAATCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAACTGGA
CAAA

FIGURE 214

MVPAAGALLWVLLLN LGPRAAGAQGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAEELLAATVSTGFSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTFPPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNLSVFTMQPIDRNQR

214/330

CCCGGCTCGACCCACGCGTCGGGGGAGAAAGCATGCCGGGCTGGCGGGCGGGTTGGTCTGCTAGCTGGGCA
GCGGCGCTGGCGAGCGGCTCCAGGAGCGACCTGTAGCGCGGTGATCCGCGAGTCCGCTAGCTGCAGTGGCGAGGAC
GAACCTGCTCTGGGGCGGCTCTGAATCACTCCGCTCCGCGACCGCAATCATAGTGAAGTTCAGAGGCTGGACCT
CTGGGACGAGCTGTAAGTATGATGTATGTGGTCACTTCCGCTGGGCTCTACTCCAGGAAGTGCACAAAGTGCCCT
CAGTTCCATGCAAGTGGCCCTTCTCCGGCTCTCCTTTCTAAGAGCGCGCATCGCGCTGGCCCTGTTTCT
CAATGGCTTGGCCAGCTGGTATGCTCTCCGCTACCGCACTCTGTCGCGAGCTCTCTCCCCCTGTACCAAC
CTGTGCTGGCTTCGCGTGGGTGCCCTCAATCATGGTTCGTGTCACAGTCTTCACACAGGAGCACTGA
CTCACAGAGAAATGGACTACTTCTGCTCCCTCACTGTCACTCACTCAATCTACTCTGTGTGCTCGAGGAC
CGTGGGCTCGAGCACCGCTGTGTGACGTGCTCCGGGCTCTCTGCTGCTACTGTCAGCTGCGACGCTCT
CTGAGCTGAGCTCATCCGCTTCGACTATGGCTACAACTGTGGGCAAGCGGCTATTGGCTGTGTCAAGTG
GTGTGTGGTGGCTGGCTGGTGGCTGTGGACACAGCGCGCGTGCTCACTGCGCAAGTGGTGGTGGTCTT
GTGTGTCGAGGGGGTTCCTGCTCGAGCTGCTGACTTCCCAACCGCTCTTGGGCTCTGGATGCCATGGCA
TTGGCACTCAGCAACATCCCTGTCCAGCTGCTCTTTTTCAGCTTCTCGAAGATGACAGCTGTACTCGT
AAGGAATCAGAGGACAGTTTAAGCTGGACGCAAGATGGAGAGCTGTGCCCAGTGGGAGTCTGCCCC
CGCCTCTGGCTGGCTTCATCTCCCTCAACCTTGAGATGATTTCTCTTTCACTTCTGGACTGGACATGA
AGGATGTGGCGGAGAAATCATGTGGCCAGCCGCCCTGTGGCCCTCAGACGCTTGGAGTCTGTTCTTAGG
AAGGCTCCCGACCTGCTGGAGCTCGAGATGGGCGACCCCTCACTCTCTGTGAAGCTGAACGTGGGTGGAGCTGA
GTGTGTTCTAGCTCTACCGGGAGACAGTGGCTGTTCTCCGCCAACGCTCTCCACACTCCCAAGCT
CTTGGCTGGTCCCTGAAGCCCTCTGTCTATCTGGGAGACAGGGAGACGACGGCTTAGGATGACAGGGGGTCC
CTTCTGTACCAACGCCACCTCTCCAGCAACAGCACTAGTGGTGCAGTGTGTTCTTTTGGCGAGCA
GGTTCACGGCGCTCTCCCACTGGATCTTGAGGACCAAGCTCTGGGATGGGAAGGATTTTCACTCTGACC
TGTGCCCTGACAGGTTCAGAGAGGCTCAGCAATCTCCCTTCAGGAGCGGAGCTCAGCAAGCCAGGGCA
AGGATCTGCTGCTGTCTGTGTGAGGCTCGCCACCGTGTGCGGAGTGTGGGCAAGCTGAGTGCATAGG
TGACACCGCTCTCAGCATGGCTGGTGTGTGTGAGTCTAGGCTAGGTGGCGATGTGGAGACGGTGTGTG
CGGGAGAGAGGTGTGGCTTCAAAGTGTGTGTGTCAGGGGGTGGGTGTGTAGCGTGTGGTATGGGAGAGCTGTG
TGGCGTGTCTGTGGGAGCATGTAGATGTGCTGACTGGCGGTGATGTGTGCACATGTGAGAGTGTGAGCAGAT
GAGGAAATCTGTCACTCAATAATCTGCTGTGGAGCGCAGCTGTGCCCAAGCGCCACTGGGCGAGAC
CAGGAGGCTCTCATCGCCAGAGCTGGCTGTGTCATGTCTCCCTGTGTGGTGGCTTTGGCGGCTCTCTCAAC
CTCACAGGTTCCCAACACAGTGGCTCCAGAGACAGCCCTCGAGGACAGGAGAAATGGGATGGC
TGGGCTCTCTCCATCTCCTTTCTCTCTCTGCGATGGCTGGGCTCTCCCTCAAACCTCTCATTCCTCT
GCTCGACGCGCTTTGGCATAGCTGATTTGGGAGGAGGAGGAGGCGCATTTACGGAGAGGCGGAGAACT
TAGGTGGTGTGTGTTTCTTCTCTTCCAGAGGCTCTTACTGTTCCAGGCTGCCCAAGGAGCGAGCGGC
ACACTATGCTGTGCCCTGTAAAGTGAAGGCTGCATTTACAGGAGCGCTTGAAGTGTCTCTGCCACAG
ATAGAAATGAGGAGGAGCTCGAGAAATCTTCATCCNAAAGCGAGCTCTCGGTTGGAGACGACTGATTTTG
CTGTGCCCTGACCCCTGTCTCTCTTTGAGGAGGGAGCATGTAGCACTCCAACTCAGGACTCGGGTG
GCCTCGGCTAGTCTTTTGTATCTGAAACTTTTAAGTGGGAGGTTGGCAGGAGTGTGCTTAATAATCAA
TCTCAAGCTCAAAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPPAVVSAFRALLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWLLAWCLWNQR
RLPHVRKCVVVVLLQGLSLLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGA
 CT**ATG**GGCTCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
 CTGATGGCCGCTGCTTCACCTTCTGCCTCAGTCATCAGAACCCTGAAGGAGTTTGCCCTGAC
 CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAAGAACCAAGCCGAGGAGGAGC
 TGGATGCCGAAGTCTTGGAGGTGTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG
 CAGGCTGTCCCTGCAGGATCCACGTACGGCTGAATCTTCAGACTGGGAAAGAGAGGCCAA
 ACTCCAATATGAGGACAAGTTCGAAATAATTGAAAGGCCAAAGGCTGGATATCAACACCA
 ACACCTACACATCTCAGGATCTCAAGAGTGCCTGGCAAAATTCAAGGAGGGGCGAGAGATG
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAGCGGCTCTTCCGCCCCATTGA
 GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTCTATTGAGACTGACATGCAGATCATGG
 TACGGCTGATCAACAAGTTCAATAGTTCAGCTCCAGTTTGAAGAGAGAAGATTGCTGCGCTC
 TTTGATCTTGAATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTG
 TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCTCGTGAAGGAGTATGCTGCGT
 TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCAGGTGGAGGCCATCGAAGGGGGA
 GCCCTGCAGAAGCTGTGCTCCCTGCTGCGCCACTTCCCTATGCCAGCGGCAGTTCTCTGAAGC
 CCTGTTTGCACTGTGCTCCCTGCTGCGCCACTTCCCTATGCCAGCGGCAGTTCTCTGAAGC
 TCGGGGGGCTGCAGGTCTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
 CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCCCAGGAGGAGGCTGA
 GCTGACCCAGGAGATGTCCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
 GCCTGTGGGAACAGGGGCTGGTGCAGATCACGGCCACCTCCTGGCGCTGCCCGAGCATGAT
 GCCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCCTGCCGGGACCGCTACCG
 TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
 GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC
 AGCTTGCTGAAGGAGCTGAGAT**TGA**GGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
 GGCTGAGGGGTGCCAGCGTGGGTGGGCTTCTCAGGCAGGAGACATCTTGGCAGTGCTGGCT
 TGGCCATTAAATGGAAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 218

MAPQSLPSSRMAPLGMMLGLLMAACFTFCLSHQNLKEFALTNPKESSSTKETTERKETKAEEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGTEVLAVRVVTLTYLDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTGGGGTTTCGGTTCCCCCCCCCTCCC
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTCGCGTTGCCACCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCC
 TTCCCACTGACCAAGCCATGGGGGGTCTGCGGTGTTTTTCGGCTGCACCTTCGTGCGGTTGCGG
 CCGGCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGGGTTATCATCTCTGGT
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCTATCTTGG
 TCCATGTGACCGACCGGTGATGCCCCGGCTCCAGTACCGGCTCCTGATTTTTGGTGCTGCT
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCT
 GATCACTTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCTCGACTTC
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTGGTGGTGGGAGTCACTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCTTCATCACAGCTGGAGGGTCCCTCCGAGTATTACAGCGCAGCC
 TCTTGTTGTAAGGACTGACTACCTGGACTGATCGCCTGACAGATCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATCTCTGTCTCCTTCTCGTCTC
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTCTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCCTGGGTTTCAAGCAGTCACTGGTGGGTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTTGTTGTGTCCAGGACTCCCCCTGTGTGAGTCTGCTCTCAC
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGCAAGCCGACGGCAGGAGGACAGTGGGTGAT
 GGTGTATTCTGCCCTGCGCATCCCAACCGAGGACTGAGGGAACCTAGGGGGACCCCTGGG
 CTGGGGTGCCCTCTCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTCTGGACAGTGCAG
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC
 AGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCTAACTGCCTTTTTTTCTTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATGGAACCTTCTAACCCTCTGGGCTATATTTCTC
 TCCTCGAGTTGCTCTCATGGCTGGGCTCATTCGGTCCCTTTCTCCTTGGTCCAGACCTT
 GGGGGAAGGAAGGAAGTGATGTTTGGGAACGGCATTAAGTGAACCTAATGTTTTAACT
 CCTTAACCAACAGCATCCCTCCTCTCCCAAGGTGAAGTGGAGGTGCTGTGGTGAAGTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAAGTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTTTGTAGTTTTTAATGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAAGTGT
 ATCATTTTCTGCTGAGGGTGGAGTGTCCATCCTTTTAATCAAGGTGATTGTGATTTTGACT
 AATAAAAAAGAAATTTGTAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0992521.11401

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLASVWVFIILVHVTDR
SDARLQYGLLIIFGAASVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIGHGDSPPYFLTSAFLTAAIILLHTFGWGVVFFDACERR
YWALGLVVGSHLLTSGTLFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTCTGTTGAGTGAGGACGGAAGATCAACCCA
 TTTCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
 TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
 TCACCCATTANTTCTTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

GACCGACCGTTTCAGATGCCGGTTCAGTACGGCTTCTGATTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNCTGAGTGAGGACGGAAGATACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTACCCATTAATAATCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGTATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTCCCTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTGCGCCCGGCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTGAGATGCCC GGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACITG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCCATTTGCCTGTCTGGTCAGGCCCCCACCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTGCGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCGAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

0992521-11404

GCCCAGGAGCAGTGGGTGTTATAACTCAGGCCGGTGCCAGAGCCAGGAGGAGCA
 TGGCCAGGAAGGCACAGGCCCTGAGAAGTCTCGCGCTGAGCTGGGAGCAATCCCCACCCC
 TACCTGGGGACAGGGCAAGTGAGACCTGGTGAGGCTGCTCAGCAGGCAGGGAAGGAGAG
 TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCATAGTGCTGGGTCTCAGCGCAGTGCCGATGGTGCCCCG
 CCTTGTGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATTGGGCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGAGCTCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGCGCGCTGTTGTCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCTATCCACAGTGCGCTGCTCAGGCCGCCCACTGCAG
 GAAGAAAGTTTTCAGAGTCCGTGCTGGCCACTACTCCTGTCAACAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCCTGGCTACTCCACCTGGCCACTCT
 CAACGACTCATGCTCATCAAATGAACAGAAGAATTCTGCCACTAAAGATGTCAGACCCAT
 CAACGCTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGCTGGCTGGGGACAA
 CCAAGAGCCCCCAAGTGCCTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCTGCCAGGGTGATTTCTGGGGGCCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTCTGGGGAGATTACCTTGTGCCCGGCCAACAGACCGGGTGCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAACCATCCAGGCCAACTCTTGAGTCTAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGTGTCAGGGACAGCCCTGACACTCCTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGCTCTCTAGTTGAACCATGG
 GAACAATTTCCAAAATGTCACGGCGGGGGTTGGGTCTCAATCTCCTCGGGGCACTTTCAT
 CCTCAAGCTCAGGGCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAGTGGAAAAAAA

FIGURE 226

MATARPPMWWLCAITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGD SGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAAAGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGGCGCGCA
 CAAGCCGAGCGGGCGAGCTGCGGCTACGTGCTGTGCACCGTGTGCTGGCCCTGGCTGTGC
 TGCTGGCTGTAGCTGTCAACCGGTGCCGTGCTTCTCTGAACACGCGCCACGCGCGGGACG
 GCGGCCACCTGTCTGTCACTGGGCTGCCAGCGCCACAGCGCCCTGGTCACTGTGGA
 AAGTGGGAGACACTCGCACTCAGCATCTCATTGACCGCGCTGCCCGAGCTCACCGACA
 GCTTCGACAGCTGGAGAGCGCCAGGCTCGGTGCTGCAAGGCGCTGACAGAGCACCAGGCG
 CAGCACCGCTGGTGGGCGACAGGAGCAGGAGCTGCTGGACAGCTGGCCGACCACTGTGCC
 CCGCTGTGGCCGAGCCTCAGAGCTGCAGAGTGAGCAGGCGCGCTCATCCAGCTTCTC
 GCACGCTGGGCGAGGCGCTCAGCGCCTGCAGAGTGAGCAGGCGCGCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTGACGACATCTGGATGCCCT
 GCAGAGGAGCAGGCGGCTGGGCGGCGCCGCAACAAGGCGGACCTTCAGAGAGCGCTGCC
 GGGGAGCCGCGCGCGGCTGTGCCATGGCTCCCGGCGCGGAGACTGTCTGGAGCTCTC
 CTAGCGGAGACAGGAGCATGGGCTTACTGTCTTCCACCCACTACCGGCGCGGCTT
 CTAGGCTGTACTGTGACATGCCAGCGGAGCGGCGGCTGGACGGTGTTTACGCGCGGGAGG
 ACGGCTCCGTGAATCTTCCGGGCTGGGACGCTACCGAGAGCGGCTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGCTCAAGAGGATCCACGCGCTGACCACACAGGCTGCCTACGAGCT
 GCACGTGGACTGGAGACTTTGGAATGGACCGGCTATGCCCGCTACGGGAGCTTCGGCG
 TGCGTGTGTCTCCGTGGACCTGAGGAAGACGGGTACCGCTCACCGTGGCTGACTATTC
 GGCACGTGAGCGGACTCCCTCTGAAGACAGCGGATGAGGTTACACACCAAGGACCGTGA
 CAGCGACCATTCAGAGAACACTGTGCCGCTTCTACCGCGGTGCTTGGTACCGCAACT
 GCCACAGCTTCAACCTCAATGGGCACTACCTGCGCGTGGCAGCGCTCCTATGCCGAGCG
 GTGGAGTGGTCTCTGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCCGTCGCGGAGGACCGCT**TAG**ACTGGTGCACCTTGTCTTGGCCCTGCTGGCTGCTGCG
 CCCATCCCGACCCCACTCACTCTTCTGTGAATGTCTCCACCCACTGTGCCTGGCGGAC
 CCACCTCTCCAGTAGGGAGGGCGGGGCCATCCTGACACGAAGCTCCTGGGCGGTGAAGT
 CACACATCGCCCTTCTCGCCCTCCCGACCCCTCCATTTGGCAGCTCACTGATCTCTTGCCT
 TGCTGATGGGGCTTGGCAACTTGACGACCCCACTCTGCTTGGCCCACTGTGACTCCGG
 TGCTGTTTGGCTTCCCTTGGCAGGATGGTGAAGTCTGCCCGAGGACCCCTTGCCTGCC
 GGCCAAATACCGGCAATTGGGACAGAGCAGGGGGCAGACAGCACCCTGGAGTCTCT
 CTAGCAGCTGGGGGAATGTAGGTCTCTCTGAGGTGAGTCTGAGGCGAGTATCTCCAG
 CCTCCCAATGCCAACCCACCCCGTTTCCCTGGTGCCAGAGAACCCAGCTCTCCCCAA
 GGGCTCAGCTGGCTTGGGCTGGGTGGCCCATCTACAGGCGCTGAGGTGAGGATGGG
 GAGCTGCTGCTTTGGGAGCCACGCTCCAAGGTGAGACCACTCCCTGGAGGCCACCCAC
 CTGTGCGCCCGAGGCTGGGCTGCGAGTCTCTTACCTGCTGTGCCCACTGTCTCTG
 TCTCAATAGGGCCCAACCATCCCCACCACTCCCGGCGCTCTCTTCTGGGCTGAGGAGGCT
 CGGGCTGCCATCCCACTTCTCTGCTTGGAGGTGGGTGGGGCGCTGCACCGTGGGGCT
 GGACTGCTCAATGGGAAGCTCTTGGTTTCTGGGCTGGGGCTTAGGAGGCTGGGATGAG
 GCTTGTACAACCCCCACCAATTTCCAGGAGCTCCAGGCTCTGAGGCTCCCCAGGAGG
 GCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAAGCTTCC
 ATTGACCGTGGCCACTGGACCCAGGCGAGGCCCGGCGCGGCGAGTGGTCAAGGGACAGGA
 CCACCTCACCGGGCAATGGGCTCGGGGGGACTGGGGCACCAGGCAAGGCGACCACTGGACA
 CTTTCTGTTGAATCTCCCAACACCCAGCACGCTGTCTATCCCACTCTTGTGTGCACACA
 TGCAGAGGTGAGACCCGAGGCTCCAGGACAGCAGCCAAAGGGCAGGCTGGAGCGGGG
 TCTCAGCTGTCTGTCTCAGAGCCTTGGACCCGCGTGCCTTACGTGAGGCCAGATGACGG
 CGGCTTTTCAAGGCTCTCTGATGGGGGCTCGAAAGGGCTGGAGTCAAGCTTGGGAGCT
 GCCTAGCAGCTCTCTCGGGCAGGAGGGGAGGTGGCTTCTTCAAGAGACCCCGATGGCA
 GGTGCCCTAGGGGTGTGGGTTCCGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAA
 AACAAATAAATTTGACTTGGCACCCTGGGGGTTGGTGGGAGAGGCGGTGTGAGCTGGCTCT
 TGTCCAGTGCCACAGGTCATCCACATGCGCAG

FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLLDTLADQLPRLARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCCT
 TGCTTCCTGAACTAGCTCACAGTAGCCGCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCCTGCTGAC
 TTTGTGCTTGGTGTCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTCTGCAGCATGTGGC
 TGAAAACTCTGTCGTGAGCTGTATAACAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGTACCAGTCTTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAACAAGAAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGCGCCCTGACAGTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAGAATGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTTCAGGATCACCAGCATTTCTGAGCTGGGTTTTATGCAGTATTTAACAGTCACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCATAATGTCTATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTTCTCTCAATGTCTAATATCACCTCCCTGTTTTTCAT
 GTCTTCTTACACTTGGTGGAAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCCAGATTGTACC
 AGCAAAATACACAAGGAATCTTTTTGTTGTTTCAGTTTCACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCCCTGTGTCCATTAAGACTCTGATAATTG
 TCTCCCCCTCATAGGAATTTCTCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTCCATTGACCCATATTTATACCTTTCAG
 GTACTGAAGATTTAATAATAATAAATGTAATACTGTGAAAAA

230/330

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

10-11-12-13-14-15-16-17-18-19-20-21-22-23-24-25-26-27-28-29-30-31-32-33-34-35-36-37-38-39-40-41-42-43-44-45-46-47-48-49-50-51-52-53-54-55-56-57-58-59-60-61-62-63-64-65-66-67-68-69-70-71-72-73-74-75-76-77-78-79-80-81-82-83-84-85-86-87-88-89-90-91-92-93-94-95-96-97-98-99-100-101-102-103-104-105-106-107-108-109-110-111-112-113-114-115-116-117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTTCAACGTGGCGACCACTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

[illegible]

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKAVRTRYISTELGIRQRLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL
QHGDDEFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAPVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALT PQGGRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAF FPMHFQAFHPGVAPPQGPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSHLVRAVEPALLQRYRAQTCSARLSEDL
YHRCQLQSVLEGLGSR TQLAMLLFEQE QGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTTAGTGAGAAAAGGAGT
 AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTATAGAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCACTGGGCGAGGGAACCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTACCGATTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCTCATTTGAAAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCGCCCCCTGAGACCTGCAGCACCATCTGTCTATGGCGGCTGGGCTGTTGGTTTGAGC
 GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGGCCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCTGGTCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCAATGGC
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAGTG
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

FIGURE 235

MAAGFLGLSARRLLAAATRG LPAARVRWESSFSRTVVAPS AVAGKRPEPTTPWQEDPEPE
DENLYEKNPDSHG YDKD PVL DVNMRLVFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCGCT
GTGGCGGGAAGCGGCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACCTTGATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTCGACCCAGCA
AGATCCAG

GC GGCGGGCTATGCGCGCTTGCTCTGCTCGTCCGTTGCTCCTGGGGCCCGGGCGCTGGTGCCCT
TGCAGACCCCAACCGCAGACGCTCGGGAGGAACTGTGATCAACCCCGCTGCCCTTCCGGGG
ACGTGAAGCCACATTCAGTTCGCGACGCGCTGGGATTGAGACTTCAGCGGGAAGGAGTG
TCCCATTACAGGCTCTTTCCAAAGCCCTGGGGCAGCTGTCTCCAAGTATCTCTACGGGA
GCTGACACTGTGTCATTCACACAAGGCTTTTGGAGGACCGATATCGGGGTCACCTTCCCTGC
AGGCCCATTCAGTGCAGAGCTTGTGGGCTGTGGTTCCAAAGACACTGTGTCATGATGTGGATAA
TCTTGGAAAGGAGCTCAGTAATGTCTCTCTCAGGGAATCTCTCGGCCCTCTCTCAACTCATCGA
TTCACCAACACAGTCACCTCCCACTGCTCTCTTCAAACCCCTGGGCTGGCCAAATGACACG
ACCATACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAACCTCACC
CCCTTGAAGAAGCTCTTGCCCTGTAGTTTCCAAGCAGGCCCTCTGTGCTGCTCGTAGGCGAGA
TCGCTTGGTACCAACGAGCTACCACTCCGAGCGAGTGCATATCCGCCCTGTTTGCAGAAATG
CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCTGTGAGTTGTATTGTATGCTCTC
ATCAGCGGGCAGGGAAGAAGACTGGTCCCTCTCCGAGTGTCTCCCGAACCCCTCACGGA
GCCCTGGCCCCCTGGCTTCAGAGAGCCGATGCTATGTGACATCAACCATAACCCAGGACA
ACGAGACATTAGAGTGCACCCACCCCGACCACTACATACAGGACGTCATCTTAGGACAT
CGGAAGACCTATGCCATCTATGACTGCTGTGACCCGCGCATGACAACACTCTGAAACACT
CAACATCCAGCTCAAGTGAAGAGACCCCCAGAGAATGAGGCCCCCCCAGTGCCCTTCTCTGC
TGTGCCAGCGGTAGCTAGGTGCTGATGGGCTGCAGAAAGGGGAGCTGAGCACACTGCTGTAC
AACACCCACCATACAGGGGCCCTTCCCGGCTGCTGCTGCTGCAGACCGTGACCTGTGATCTGCG
GCTGTATGTGCACACCCCTACCATCACTCCAAGGGCAAGGAGAACAAACAAAGTTACATCTC
ACTACAGCGCTGCCACGAGGACCGGCTGCCAACCCCACTCTGGAGATGCTGATTCACTGCGG
GCCAATCAGTCACCAAGGTTTCCATTCAGTTTGAAGCGGGCGCTGCTGAAGTGGACCGAGTA
CAGCGGATGCTCTTACCAATGGCTTCTATGTCAGGCCATCTGTCTCAGCGCCCTTGTGGCCCA
GCATGGTAGACCGCAAGCTGAGCATGTGAGTATGGGAAGAGGATCCCTCTTCAACAGCCTGTCTCCA
GTCTCTGATGGCTCTAACTACTTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
GACACCGGACTCAGCATGCCCTCAACGCTGATCTGCTCAGCTGCACTGTGTTGGCCGTGT
GTACAGGCTCCTTCTACAATCTCTCACCGCAACCTTCCATCTGAGGAGGCCCGCAGAGT
GGCTTGGCAAGCGAGCTGGCCAACTTATCCGGCGCGCCGAGGTTGTCCCCCACTCTGTAAT
CTTGCCCTTCTCCAGCAGCTGCAGCTGCGGCTTTCTCTCTGGGAGGGGAGCCCAAGGCTGTT
TTCGCCATCTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCGAGTCAAGGC
CTACAGCTGTGTTTCTCCAGTACAGGAGCCAGGAGCAAAATGTGGCAATTGAAATTTGAAATTA
CTTAGAAATTCATTCTCACTGTAGTGCCACCTCTATATTAGGTGCTCAATGAAGCAAA
AGTGGTCCGGTGGCTGCTGTATTGGACAGCACAGAAAAGATTTCATGACACAGAAAGGTC
GGCTGGCAGCACTGCCCAAGGTGATGGGGTGCTACACAGCTGATATGCTGCTGTAGTGGTA
TGGAGTTTACTGTTTGTGAATTAATAAACGCGCTGTTTCCGTGGAAAAAATAAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDKSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSSISWELRQTLSVVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTVFWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSQIFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLTPDFSMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAAATGATGCTGGGTCCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCCTGAGACTTGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCAGGGACGGTACTTCCCTCTCTACCTGGTGTCTCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCACTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAAGTGAAGAAATAAATAT
TTGCTGTTTATAATCCAA

240/330

FIGURE 240

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGTTGTCACCTTCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACCA**TC**AGGTCCTGCCTGTGGAGATGCAGGACCTTGAGGCCAAGG
 CGTCCAGTGGTCCTTGCTTCGGCTGTCTGGTCTTCTTTCTCTGGCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAAACAAAGCCTTCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTC
 CTACAGTCCCTGGCAAAGCCTTAAGTCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAACCCAGCCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAGACACCCAAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTCAGAGAAGCACAGGGCAAGCGGCCAACACAGCCAAGACGCTCATTTCCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCATCTATCCACCTAAGGAGAAGAAACCTCAGGGCACCCACCCCTGCCCCCTTTCCAG
 AGCCCCACGACGACAGAGAACAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAATACAGCTTCGAAATAGGAGGGCTTCAGACGACTGCGCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTTGCCCAACCTCACTCTC
 TTCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAAACACTTTGCACCACC
 CTTTGGCTTCAGAGCTCAACTACTCCTTGGTGCAAGGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGATCACCTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTCGATTGAGCGGAGCTCTCATTAAGGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTATATTGGGCAAT
 CGGGGTTCAGAAACGTGCTCCTTGGGAAGGACGTCCGCTACTTGCACTTCTCGGAAGGCAC
 CCGGGACTATGAGTGGCTGGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCAGAACCTGGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGATAATCCGGCTGTACCAGGCTCCTGGTC
 CCGGAACTGCCAAAGCCAAAGAACT**TC**AGCGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC
 CAAGGCACAGGATACAGTGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA
 GCTCCAAGCCTTCAGGAGTTTCAAGGGAAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAATGGCTAAATTGAGGTTCTGAAGTCTTTCAGTACATTGCTGTAGGTCCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAAATACCAACAATTCTCGCTGAAAAACACTCTT
 CCAGTCCAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAACATATAGATCTG
 GTTGAATTCAGATCGAGTTTACAGTTGTGAATCTTGAAGGTATTACTTAACTTCACTAC
 AGATTGTCTAGAAACACTTTCTAGGAGTTATCTGATTTAGAAGGCTATACATCTGTCCTTG
 TCTTTAAGCTATTTGACAACTCTACGTGTGTAGAAAACCTGATAATAATACAAATGATTGTT
 GTCCATGGAAGGCCAAATAAATTTTCTACAGTGAAAAAAGGAAAAA

MRSCWLRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTEINIKERSLQSLAKP
KSQAPTRARRRTTIYAEPAPENNALNTQTQPKAHTTGDGRGKEANQAPPEEQDKVPHTAQRAAW
KSPEKEKTMVNTLSRPGQDAGMASGRTEAQSWKSQDTKTTQGGNGQTRKLTASRTVSEKHQG
KAATTAKTLIPKSQHRLAPTGAIVSTRTRQKGVTTAVIPPKEKKPQATPPAPFQSPPTQRN
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKFLFLPNLTLFLDSRHF
NQSEWDRLEHFAPPFGMELNYSLVQKVVTFRPPVPQQQLLASLPAGSLRCITCAVVGNGG
ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFTAFSLTQSLILGNRGFKNPV
LGKDVRYLHFLGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREAHMDRYLLHLPDFL
RYMKNRFLRSKTLDGAAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDDHYDTSW
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

CGATGCGCGGACCCGGGCACCCCTCTCTCTGGGGTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGACAAGTTTCTAAAACCT
TACAGGCCCTCTTTATTTAGTCCAAAGTCGACAAACACTTCCATAGACTTTATCAACA
CCAGAGACTGCACCATCTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGCTGGCT
GTCAGTCCAGTGTGCATGAGGATAAGTGAAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCCTGGAAACCAACAGGGAAACGAACATCTTTATACACTCCCCTCATGG
ACAAGAGATTATTTTTGCAGACAGACTCTTCCATAAGTCCTTTGATCTTTGATGTGTG
ACAGTTTGCAGATATATATGATAAATCAGTGACTTGACAGGTTATCTGTCACTTATT

244/330

FIGURE 244

MRGPGHPLLLGLLVLGFSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMDK

090551-11401
10477-122000

FIGURE 245

GGGCTGGGCCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCTCGGGTCCCTTCTCTGGGAGG
CCCGACCCCGGCGCGCCAGCCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGCGCCG
CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCCTGGTGCTGGCCGGCGAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTCACCTTCT
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGAG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCTCTGTTCTGTTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTACCCGGGAGCC
TGAAGGAACCAGCCATGTCTCTGCTGCCCCCTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCTGGGGGTGGCAGGAGTCCCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAAC TAGA
ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGCAAGGGAGG
GAGATGACAGCCTGGGTACAGTGCCTGTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAA

FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSPGAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGCGCGCAAGGGTGAGGGCGGCCCCAGAA
 CCCCAGGTAGGTAGAGCAAGAAAGATGGTGTCTGCCCCCTCAAATGGTCCCTTGCAACCATGT
 CTATTTCTACTTTCCCTCACTGTTGGCTCTCTTAACCTGTGCCACTCCCTTCATGGTGTGAGAG
 CACTGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCTTGGAAATAAAAATACGACTTCT
 CTGAGTAGCTCATCCGATCTCATTATGATCTCTTGATCCATGCAAACTTCCACGGTGCAC
 TTCTGGGGAAACCCAGAAAGTAGAAATCACAGCCAGCTCAGCCCAACAGCACCATCTCCTGCA
 TAGTACCACCTGCGAGATATCTAGGGCCACCCTCAGGAAGGAGCTGGAGAGGGCTATCGG
 AAGAACCCCTGCGAGTCTTGGAAACCCCCCTCAGGAGCAAAATGCACTGCTGGCTCCCGAG
 CCCCTCCTGTGCGGGCTCCCGTACACAGTTGTCTTCACTATGCTGGCAATCTTTGGGAGAC
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGCTGAGGATACGTAGCAT
 CAACACAATTTGAACCCACTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC
 AAGCGAAGTTTCTCAATCAAATTAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTGATGTCACTGTGA
 AGATGAGCACCTATCTGGTGGCCTTCATCATTTGAGTCTGTGACGAAAGATAAC
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGC
 ACTGGATGCTGCGGTGACTCTTCTAGAATTTTATGAGGATTATTTGACATACCGTATCCCC
 TACCCAAACAAAGATCTTGTGCTATTCCCGACTTTTCACTGCTGATGGAAAACCTGGGGGA
 CTCGACAAATATAGAGAACTCTGCTCTGTTGTTTGTATGACGAAAAGTCTTCTGATCAAGTAA
 GCTTGGCATCACAGTACTGTGGCCCATGAAGTGGCCACCAAGTGGTTTGGGAAGCTGGTCA
 CTATGGAATGGTGGAATGATCTTTGGCTAAATGAAGGATTGGCCAAATTTATGGAGTTTGTG
 TCTGTGAGTGTGCCATCCGCAACTGAAAGTTGGAGATTATTTCTTGGCAAAATGTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCCCTGTGTCTACACCTGTGGAAAATCCGT
 CTCGATCCGGGAGATGTTTGTATGATGTTTCTTATGATAAGGGAGCTGTATTTCTGAATATG
 CTAAGGAGATATCTTAGCGCTGACGCATTTAAAGATGGTATTGTGACATGATCTTCCAGAAGCA
 TAGCTATAAAATACAAAACAGGAGCACTGTGGGATAGTATGGCAAGTATTTGCCCTCAG
 ATGGTGTAAAAGGGATGGATGGCTTTTGTCTGAGAAGTCAACATTCATCTTCACTCCACAT
 TGGCATCAGGAAGGGTGGATGTGAAAACCATGATGAACACTTGGACACTGCGAGGGGGTTT
 TCCCCTAATAACCATCACAGTGAAGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGGCTCTGACGGCGGCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTCATCAC
 AGCAAAATCCAAACATGGTCCATCGATTTTGTCTAAAAACAAAACAGATGTGCTCATCTCTCC
 AGAAGAGGTGGAATGGATCAAATTTAATGTGGGCATGAATGGCTATTACATTTGCTATTAG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACAGCAGTGTGCTCATCTCC
 AAGGTTGAATGAGTGAATCTTCTATGATTAAGTTAATGGAGAAAAGAGATATGAATGAAGTG
 GAAACTCAATTTAAGGCTCTCTCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG
 GCAGACAGGGGCTCAGCTCTCAGAGCAAAATGCTCGGGAGTGAACACTACTCTCTCGCTGTG
 TGCACAACTATCAGCCGTGCGTACAGAGGGCAGAAGGCTATTTTCAAGAAAGTGAAGGAATCC
 AATGGAAACTTGAAGCTGCCCTGTGCGAGTGAAGTGGCAGTGGTTGCTGTGGGGGCCAGAG
 CACAGAAAGGTGGGATTTTCTTTATAGTAAATCATGATTTTCTTTGTCCAGTACTGAGAAAA
 GCCAAATTTGAATTTGCCCTTGCAGAAACCAATTAAGGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAATAAAAACTCAGGAGTTTCCACAAATCTTACACTCATTGG
 CAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAGGAAAACTGGAAACCAACTGTG
 TACAAAAGTTTGAATTTGGCTCATCTTCCATAGCCACATGGTAAATGGGTACACAAATCAA
 TTCTCCACAGAAGACCGGCTTGAAGAGGTAAAGGATTTCTGAGCTTTTGAAGAAAATGG
 TTCTCAGCTCCGTTGTGTCCAACAGACAAATTGAACCAATTGAAGAAAACATCGGTTGGATGG
 ATAAGAATTTTGTAAAAATCAGAGTGTGGCTGCAAGGTGAAAAGTGTGAACGTATGTAAAAA
 TTCTCCCTTGTCCCGGTTCTCTTATCTCTAATCACCAACATTTTGTGTGAGTGTATTTCAA
 ACTGAGATAGGCTTTTGGGCTCCAACTGGAGATCTTTTTCCTTCAACTCATGTTTGTGA
 CTATCCCTGTGAAAGAAATAGCTGTTAGTTTTTCATGAATGGGCTTTTTCATGAATGGGGCTA
 TCCTACCATGTGTTTGTGTCATCACAGGTGTGGCCTGCAACGTAACCCATGATGTGGT
 TCCCTGCCACAGAAGAATAAAGTACCTTATTTCTTCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTFPPWNKIRLPEYVIPVH
 YDLLIHANLTTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLE
 HPPQEQIALLAPELLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSLYLVA
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELHQWFGNLVMTMEWWDNL
 WLNIEGFAKFMFVSVSVTHPELKVGDFYFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGMDG
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYIIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLEKMRDMNEVETQFKAFLIRLLRDLIDKQWTWDEGSVSEQMLRSELLLLACVHNYPQCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTESQIEFALC
 RTQNKEKLQWLLDESFKGDKIKTQEFFQILTIGRNPVGYPYLAQWFLRKNWNKLQKQFELGS
 SSIAHVMVGTNNQFSTRRLREEVKGFSSSLKENGSQLRCVQQTIETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGGTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
 GGCTCTCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATGGGCCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTATCGGGGACCACCATTATGACACACGGAAAC
 TTGGCTCAAGAACCACCTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTG
 CTACCTGTGTGACGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTGTTATGATGGGTACATTCACTCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTCAGGGCTGCGTGGCCCAACCTCCAGCTTCTTGTGAACCACACCAGACAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGGCCTTCTGCTTAACTCTATTACCCCCACGATTCTTACCGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCACACACAATCATTATCTACTCACCTAACAGCA
 ACACTGGGGAGAGCCTGGAGCATCCGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 250

MSAVLLALLGFIPLPGVQALLCQFGTVQHVWKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPPQGCN
LLNGTQEIGPVGMTENCNRKDFTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL CNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWVG LALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
 CAGC**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCCTTCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCGTCA
 TGGTCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTTCATGTGTGAGTTTGACAAG
 GAGAACAT**CTGA**CGCTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTCTGGGGTGTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTCTCCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

FIGURE 252

M R G N L A L V G V L I S L A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G P P G P N G E P G L P C E C S Q L R K A I G E
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N
G L M A A Y L A Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S
G G W N D V A C H T T M Y F M C E F D K E N M

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TFCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCC
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
 ATCCCCGAGAGCAGAAATAGGTACTCCACTTCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTACCTTTCTCTTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT
 CCTACATTAAAAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTTCATATGAA
 AA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKRDMDHDFVGLMGKRSVQPEGKTGPFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCTGGTGTTGTCATCCCCCTGGGGC
 TGCTGTTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGCTCACTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGTGGGGC
 CTGGGCCACCGCCTGCTCTGTTCCCGAGCCAGCTCTGTTCCCGAGCCAGTGCGTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTCCACTTGGAGAGTCCTTCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCCGCACAGACTGACCTGCGTGGTTGCCATGACT
 CTTTGCTAAACCGGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGTCAACCCCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGAAACTTCTCTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGCCCATCCGTCACTATGAATGGCTT
 TTTAAACAAACCCACGTCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTAGGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAA

MSCVLGGVIPLGLFLVCGSQGYLLPNVTILLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGR
GG SRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Signal peptide:

amino acids 1-22

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

AAGGAGAGGCCACCGGACTTCAGTGTCTCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGCGCG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCTG
TGTCTTCTTGCGCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCCCACCCTCCTGAGTGGCAATAAATAAAATTGGTATGCTG

258/330

FIGURE 258

MGSGLPVLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSGTS
VTLHHARSQHHVCNT

0992521.11401

FIGURE 259

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAACTGTTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCTCCC
CTCCGATTGTCTTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTAGCC

260/330

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

090251.14404

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
CAGAGAGCCAGCAGATAGAAGATGCGCCTGCTTGGTGTTTTCGAGGATGAAGTGTGGCCCTT
CGAGGAGCTTCTGCATTGCTGGTTCTGTTCTTTCGAGCTTTTCTGCCCCCGCCGAGGTGATC
CCAGGACCAGGCATGTGTGCATTACATCTACCAGCGCTTTCGAGTCTTGAGCAGAGGCGTGG
AAAATATGTACCCAAAGCAGCAGGGCGATACATTCAAGATTTCAAGAGTTCTCAAAAATAATA
TTGTGTCATGCTGGGAAGATGTCAGACCTACACAAGTGAATCAAGATGTCAGTGGGTATCTT
GGCATTGAGAGTTGAACGCTGCCAACCGGAGATTGACATACATCAATAACCTTCGAGAGGCTC
ACGAGTGCATCGTACAGAGCAGACATCGGCAGAAATTTGCTCCAAGAAGCTGAAGATC
TGAGAAAAGATCCGGCATCTGCTGATGCAAGCTGTGACAACTGCTGTGGGCATAAAGTC
TTTGAATATGTGAAGAAGATGATGACACACATGGCTCTTGGATGAAGATGCTGCTCTATA
ACTCTCCAAGGTGACTATTATAATTTGGATCCAGAAACACACTGTTTGGGAATTTGCAAAAC
ATACGGGCATTCATGAGGATAACACCAAGCCGACTCCCGCAAGCAAACTCTCAACTATTTTCT
CTGGCAGGGAACAGGCCAAGTGATCTCAGAAGAGGACTCTGGAAGATCGAATGCTGCTCCCA
CTAATGAGATAATCAAAATATCACTCGAAGAAGAGACTCTGGAAGATCGAATGCTGCTCCCA
GGAGGCTGAGCCGAGCATTTGGTTTACCAGCATCTCCCTCAACTTACATTGACCTGGCTGT
GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCATGAGCCATTTGGTCTCA
CAAAATGTAGCGCGGCACACTGGGAAGTGAGCAATTCATGGATACCCCATCGAGAAGCCAG
GATGCTGAAGCCTCATTTCTCTGTGTGGGTTCTCTATGTGTCTACAGTATCGTGGGCCA
GGCCCTCATCGCATCACTGCATCTATGATCCACTGGGCATACAGTAGGAGGACATTCG
CCAATTTGTTCTCCCAAGACCAAGAAGTCACTCATGATCTCATTAACCCAGAGAGA
AAGCAGCTCTATGCTGGAATGAGGAAACAGCATTTTACAACCTCCAGACAAGAGAA
GCTGCCCTGGAATGAAGTCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT
TCAGGACAGCTGAGGCTATAGCCCTTACAATATAGTATCCCTCTCACTACACACAGGAAG
AGTGTGTAGAAGTGAATACGTATGCTCTTTCCAAATGCTACTGCTTAGTATCTTC
CAAGAGCTTAGATGAGACATATCATCAGAAAGTTTCAACAATGCTCCATTACTCCCCAAA
CTCTCTGGCTCTCAAGTAGACCACTTCTGATACAGGCTACTTCAGCGCTTTGTTTACT
GCTCCCGAGCATTTACTGTAACTCTGCCATCTCCCTCCCAACATTAGAGTTGTATGCCAGC
CCCTAATATTCACCACTGGCTTTCTCTCCCTGGCCTTTGCTGAAGCTTCTCCCTCTTTT
CAAAATGCTATTGATATTCTCCCAATTTTCACTGCTCAACTAAAATCTAATATTTCTTT
CTTTTCTTTTCTTTTTCGAGACAAGGCTCACTATGTTCCAGCGCTGGTCTCAAACTCC
AGAGCTCAAGAGATCTCTCGCTCCGCTCACTAAGTACCTGGGATTACAGGCATGTGCCAC
CACACTGGCTTAAATATCATTTTCTTATGAGGTTTAACTCTATTTCCCTAGGCCCTGTC
CTTCTCAAGCTTGGTAGATGTTAATATAAAGTGAAATATTAACATTTGAATATCGCTTT
CCAGGTGTGAGTGTTCGACATCATTTGAATTCGTTTCACTTTTGTGAACATGCACAG
TCTTTACAGCTGTCACTTAGAGTTTAGTGAGTACACAATTAACAAGTGAAGATACAGC
TAGAAAACTACAAATCCCATAGTTTTCATTCGCCAAGGAAGCATCAATACGTATGTT
TGTTCACTACTCTTATAGTCAATGCTGTCATCGTTTCAGCTTAAATATAGTCTGTGCC
TTTAGCCAGTTTCACTGCTGCACAAGACCTTCAATAGGCCCTTCAATGTATGATTTCTCC
AGAAAACCAAGTCAAGGCTGAGGACCCCACTAGCTCTCTCTGTCTGCTGCTCTGCT
TTCTCTCTTCTGCTTTAAATTCATAAAGTGACACTGAGCAAAAAA

FIGURE 262

MMVALRGASALLVFLAAFLPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYERFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEKKKIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPPTLGVEHSDWT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

000001-1101
100000-120000

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFI VWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNTHAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHKLRASNESTRQLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTTGCCACGCGAGTCTCAATCATGCTCC
TCCTAGTAAGTGTGTCTGACTGTGCTGTGATCACAGGGGCCCTGTGAGCGGGATGTCCAGTGT
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGGCACAAGTCCCCTTCTTCAGGAACGCA
AGCACACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGTTCCCGGACGCGAGGTAC
CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGCGCTTGCCTGGTCTCAGGATACCCA
CCATCCTTTTCTGAGCAGAGCCTGGATTTTATTCTGCCATGAACCCAGCTCCCATGAC
TCTCCAGTCCCTACACTGACTACCTGATCTCTTGTCTAGTACGCACATATGCACACAG
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
CTGTGGTGTGAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
AATGCGAGAAAGGACATTCCCCCTCCCTCCCAAGGTGACCTGCTCTCTTCCCTGGGCGCTG
CCCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
GCATTGCTCAGAGTCCCAGGTCTTGCCCTGACCCCTCAGGCCCTTCACGTGAGGTCTGTGAG
ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
TCAAGATTGGCTCTTCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAAGTCAGCCTGTGGCTTGTGGCTGTGA
CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGGCCCCCTCTTACCACACTTTACCA
TAACCACTGAAGCCCCCAATTCCACAGCTTTTCCATTAAATGCAAAATGGTGGTGGTTCAA
TCTAATCTGATATTGACATATTAGAAGGCATTAGGGTGTTTCCCTTAAACACACTGTTCCCA
AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGTCAGTCTCTGTCTCAGATTGGGG
TGGGAGCAAGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTAGACACCAGGGAGG
CAACTACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCTTTC
 CTCCAGGACCCAAGTTTCTTACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCTTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT
 GATGTTTATGGGATTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCTGTGTGGGATCA
 GGAAAGCAGGCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCAAGACTTTGGCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGATT
 GTTTCCTCTGTCCTTAAGGAGTGAGAAACCCATTATATACTCTACTCTCAGTATGGATT
 TTAATGTATTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAACTCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACCTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

MSFLQDPSFMTMGWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSLMDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRKMMFMFGIRLGVVYNFFRAWNGGFSGNLEGEFGILGGVFV
VGSGKQIGILLEHREKEFGDKVNLVSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTGCGAGGTGCCCCCTGCCCCGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTCCTCGGCGCTGCCAACC CGCCACCCAGCCCATGGCGAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGCCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAA

FIGURE 270

MANPGLGLLLALGLPFLRLRWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIV
VFSLLAALLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

[illegible]

FIGURE 271

AATATATCATCTATTATCATTAAATCAATAATGTATTCTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTCTGTCACTATTATTATGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCAAGGAAAAAAAAA

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLD SRGLILGAEAWGRGVKKNT

FIGURE 273

CCGAGGAATAACTAGAGAGGAACAATG GGGTTATTTCAGAGGTTTGTGTTTCCCTCTTAGTTCT
 GTGCCCTGCTGCACCACTCAAATACCTCCTTCATTAACTGAATATAAAGGCTTTGAAGATA
 TTGTCTATTGTTATAGATCCTAGTGTGCCAGAAGATGAAAAATAATTGAACAAATACGAGGAT
 ATGGCTACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA
 TGTATCTATATAATTCTGAGAAATGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAACTATG
 AAAACCTATAAATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTACAGAATGTGGAGACAAAGCGAATACATCTCACTTCAACCCCTGACCT
 TCTACTTGGAAAAAACAATAATGAATATGGACCACCAAGGCAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTCTACCCGTGCTAAG
 TCAAAAAAATCGAAGCAACAGGTTGTTCCGCAAGGTATCTCTGGTAGAAAAAGAGTTTATAA
 GTGTCAAGGAGGCACTCTCTTAGTAGACATGCAGAATTGATTTACACAAAAAAGCTGTATG
 GAAAAGATTGTAATTCTTCTCTGATAAAGTACAAAAAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATCTCTGTGTTGAATTTTGAACGAAAAACCCATAATCAAGAAGCTCCAAG
 CTAACAAAAACATAAAGTGAATTTTTAGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATT
 TTAACAAACCATATCCCATGGTGACACCACCTCCTCCACTGTCTCTCATTTGCTGAAGATC
 AGTCAAAAGAAATTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAGGACCGCT
 AAATCGAATGAATCAAGCAGCAAAAAACATTTCCCTGCTGCAGACTGTTGAAATGGATCTGGG
 TGGGATGGTCACTTTGATAGTACTGCCACTATTGTAATTAAGCTAATCCAAATAAAAAAGC
 AGTGTACAAAGAACACACTCATGGCAGGATTACCTACATCTCCTGGGAGGAACCTTCCAT
 CTGCTCTGCGAATTAATATGCAATTCAGGTGATTGGAGAGCTACATCCCAACTCGATGGAT
 CCGAAGTATGCTGCTACTGATGGGAGGATAAAGTCTGCAAGTTCTGTATTGATGAAGTG
 AAACAAAGTGGGGCTATTGTTGATTTTATGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAT
 AGAGATTGAGCAAGATAACAGGAGGAATCATTTTATGTTTTCAGATGAAGCTCAGAACAATG
 GCCTATTGATGCTTTTGGGGCTCTTACATCAGGAAATACATGATCTCTCCAGAAAGTCCCTT
 CAGCTCGAACTAAGGATTAACACTGAATAGTAACTGCTGGATGAACGACACTGTCTATAAT
 TGAATGATCAGTGGGAAGGACAGCTTCTTCTCATCACATGGAACAGCTGCTGCCCTCCAGTA
 TTTCTCTCTGGGATCCAGTGGAAACATAATGGAATTTTCAAGTGGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATCCAGGAACCTGCAAGGTGGGCACTTGGGCATACAACTCTTCAAGC
 CAAGAGCAACCCAGAAATTAACATTTACAGTAACCTCTCGAGCGCAAAATCTTCTGTGC
 CTCCAATCAGAGTGAATGCTAAATGAATGAAGGACGTAACAGTTTCCCAGGCCAATGATT
 GTTTACGCAAGAAATCTCAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTTAT
 TGAATCAGAGAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTACAGCATATACAGAAAAATGGCAGATAT
 AGCTTAAAGATTCCGGCTCATGGAGGAGCAACACTGCCAGGCTAAAAATACGGCCTCCACT
 GAATAGAGCCGCGCTACATACAGGCTGGGTAGTGAACGGGGAATTTGAAGCAACCCGCAAA
 GACCTGAAATTTGATGAGGATCATCAGACACCTTGGAGGATTTCAGCCGAACAGCATCCCGGA
 GGTGCAATTTGGTATCACAAGTCCCAAGCCTTCCCTGCTGACCAATACCCACCAAGTCA
 AATCACAGACCTTGATGCCACAGTTTATGAGGATAAGATTATTTCTACATGGACGACCCAG
 GAGATAATTTGATGTTGGAAAAAGTTCAAGTTTATATCATAGAATAAAGTGCAAGTATTTCT
 GATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACACTGATCTGTCACCAAGGA
 GGCCAACTCCAAGGAAAGCTTTGCATTTAAACCAGAAAAATCTCTCAGAAAGAAATGCAACCC
 ACATATTTATTTGCCATTAAGATATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATT
 GCACAAGTAACTTTGTGTTTCCCTCAAGCAAACTCTGATGACATTGATCTACCTACCTCTCC
 TACTCTTACTCTTACTCTGATAAAAGTCATAATTTCTGGAGTTTAAATTTTCTACGCTGGTAT
 TGTCTGTGAATTTGGGCTGTTGTAATTTGTTAACTTTATTTTAAAGTACACCACTTTGAACCTTA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAACCAATGTAAGT
 AAAGGATTTTCTGAATCTTAAATTCATCCCATGTGTGATCATAAAACTCAAAAAATAAT
 TTAAGATGTCGGAAGAGGATCTTTGATTAATAAAAAACACTCATGGATATGAAAAACTGT
 CAAGATTAAAAATTAAGTACTTATTATTTGTTATTTTATTTGTAAGAAATAGTGAAGC
 AAAGATCTTTTTCATACGATACCTGGTTGATATTTATTTGATGCAACAGTTTCTGAAAT
 GATATTTCAAATTCATCAAGAAATTAATCATCTATCTGAGTACTCAAAATCAAGTAAA
 GGAGAGCAAAATAACAACATTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 274

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGGSCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDfKNTIPMVTPPPPPVFSLKKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAAKHFLQLTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGDNNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMKNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYSLKVRAG
 GANTARLKLRLPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTLDFSRASGGAFFVVSQV
 PSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDNFDVGVQRYIIRISASILDRLDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

[illegible]

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIES
ALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMANTLINIVPLAKRVDFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIIYGHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEVDHLYRKYLSNLIVVRTPVRLFLHLWHEKRCMDELTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

GGAAGAATGTTGTGGCTGCTCTTTTTCTGGTGACTGCCATTGCTGAACCTGTGCAAC
AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
ATGCGCTGGGATACCAATGAAGAATACCTCTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC
AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAT
CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCATCTG
GATTATTATATTGGTGTGATATTTGCATCATCATAGTTGCAATTGCACACTGATTATTTAT
CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
AAGTGTGAAACATGATCACAAATGAAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG
GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
TGTTCTGCTTCTCAAGAAATTAACATTGTGTTCTGTGTGACTGCTGAGCATCTGAAATA
CCAAGAGCAGATCATATATTTTGTTCACCAATCTTCTTTTGAATAAAATTTGAATGTGCT
TGAAAGTGAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC
TCAAAATATCTTAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTC
AAAGACCTAAGGAAAAATAAATTTCCAGTGAGAAATACATATAATATGGTGTAGAAATCAAT
TGAAATGGATCCTTTTGCAGCATCACTTATATCACTCTGTATGACTAAGTAAACAAAG
TGAGAAGTAATTATTGTAATGGATGGATAAAAAATGGAATTACTATATAGAGGTGGAAAT
TTATCTGTTATCACACCAACAGTTGATTATATATTTCTGAATATCAGCCCTAATAGGAC
AATTCTATTGTTGACCACTCTTACAATTTGTAAGATCCAATCTGTGCTAACTTAATAAAG
TAATAATCATCTCTTTTTAAAAA

AACCTCAAACCTCCTCTCTCTGGGAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
CCTATAGCAGCTGTGGAAATTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
TCGGTTAAAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
CAACCCATGAGTGGGCGGTTTAAGGACCGGTGTCTTGGGATGGGAATCCTGAGCGGTAGCA
TGCCTCCATCCTTCTCTGAAACTGCAGTTGCAGACAATGGGACATACACTGCCAGGTGA
AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCTGTCACACTGTA
CGCTTCTCTGAGATCCACTTCTTGGCTCTGCGCCATTGGCTCTGCCTGTGCACTGATGATCAT
AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
ATAAAGTGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGACAA
GAACCCTAGTATTTCTTGAAGTTAATGGAACCTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
TTTCCAACCAAGTTCTGCAAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
AGTGTCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTATTATTAATTCAGA
GTGTAATAATTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGGCCTTAA
GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAGCC
AATTTGTCTGTACATTTCCCTTTACAGTATTTCTTTTAGCAGCACTCTGCTACTAAAGTTA
ATGTTGTTACTCTCTTTCCTTCCCACATTTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTG
TTCTTGATTAAACAGTAAATCTAAATTCAAACTGTTAAATGACATTTTATTTTTATGTCTC
TCCTTAACATAGACACATCTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
TTTGTCG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQVFVYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDNNGTYTCQ
VKNPDPVDGVIGEIRLSVVHTVRFSEIHFLALAIQSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEEERLNQEKKVSVYLEDTD

[illegible]

FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTCATGCTTCCTGTGATTTC
ATCCAACTACTTACCTTGCCTACGATATCCCCTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACCGTGGCCTGGTCCCTCCTTGGCCGAGAGA
GTGTCCTGGGTGAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGCCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAAAAACCACAGGCTGG
ATTTGCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAAAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCGTGAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAGACCAGCCTGGCCAAATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWSVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCCWPFVGVARGGALCQ

050511-110

FIGURE 285

GTC**ATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
 GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
 GACCTTGCACTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGGTGACAA
 AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTGAGC
 CGGGGCCGGGATGCAGCCAGGAACCTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
 AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
 GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
 CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
 AGATCCAGGAGAGACTCCACACAGCGCGCTCCAGCCT**TGA**ATCTGCCTGGATGGAACAGT
 GACCAATCATGCTGCAAGGAACACTTCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
 CCTGTTCACTGGGATCAGCCAGGGCGCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGTGGAGGAAGGACATGTA
 CCCTTTCATGCCTACACCCCCCTATTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGATGGACTTGTAAATTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCGATTAAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTTACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAGGAGGAATCCTGGTTATCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAAGTGTCTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATACATATGCGAGTTTACCATCCC
 TAAAT**TAG**GCTCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATATTTTACTTATTAAAAAATTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTTCTGCCATGTCTGGCAATAATACC
 TTGTCAGCCCATTAACCTTATTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGAAGCTGAAAAGTGAATTTAAAGAATGCTATCTTGGAATTTGCATACGTCTGTGCAATT
 TTTTATTTCTGCCTAGTGCATTCTGCTTGTTTAACTAGATTGTACAAAATAAATTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGGAAATGGGCTTTTGAAGCAAAACAATTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACCTTAACTACACATGCTTGGAATTAAGTTTTAGCTGTTTTTCATTGCTCA
 ATAATAAAGCCTGAATTCGTATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNNGKRENCVLFSSAQGK
WSDEACRSSKRYICEFTIPK

GCAGGAGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCGCAGGTTCCCCGCGCGC
CCCGAGCCCCCGCGCCATGAAGCTCGCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCACGCTGTGCTGCGCTG
GAGTCGGCGGGCGAGGCCGGGGCCGGACCTGGCCAACCCCTCGGCACCTCAACCCGCT
GAAGTCTCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACTCATAGAGGGCTCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGCTTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACC CGCAGGGGTGAAAAACCCGCGCGGGGAGGACCGTCCATCCCTTCCCCGCGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

290/330

FIGURE 290

MKLAALLGLCVALSCSSAAFLVGSAPVAPVAALESAAEAGAGTLANPLGTLNPLKLLLS
SLGIPVNHLEGSQKCVAEELGPQAVGAVKALKALLGALTVFG

0902521 11401

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAC
 CTTTGGGCTCCGCGAGCCGATCACATGAAGGTGGTGCCAAGTCTCTGCTCTCCGTCTCTCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCCGAGCCCC
 TCAGAACCCAGACCAGCAGGTAGTGCAGGCTCCAGGGAGGAAGAGGAGATGAGCAGAGGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTGACGCTGCTGCCAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG
 CCCGGGCTCTGCTTCCCTCTTTAAGGGACTCAGAGAGACCCCTCTCCCGCAACCTGGAAC
 TGGGCTCTCACAGGGGAGTTTGGCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAAACAAAGAGACTCGGGGGAAAAATCCCAAAC
 GTTTGATGAGATTAATCCTGAAACCAAAATTAATCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCCGTGCTTTCACCGAAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCTCCACCTTTGACAAGAA
 TTTTCGTGTGATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA
 TGGAGAAAATGGGTGACCACTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAACCAGAAACATGGAAGTTTCTTTCGGAAGTTCAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAACTCTTCTACCCCTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCATGAGGCAGTGGCAGGAATCTGTGCAGAAATAC
 TGCTTATTCATGCTCTGTGATCAAAGTGGACCGGCCATTTCAATTCATGATCATATGAAG
 AAACCTCTGGAATGCTTCTGTTCTTGGGCAGGGTGGTGAATCCGACTCTCCTATAATTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTCTTTTGTCTTAAGTATGTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTCTTCTACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAAACAACATTAAAGTAAAA
 TGAAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGCGAGGAGCATAGACAGTGTGGAGACATTTGGGCAAGGGGAGAATTCA
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCATCCCACTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTCAATTTAATGTTTTGGACCATGGT
 TGACCATGGTTAACTGACATGCAGAAAGCAAACCATGGATAAGGGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

0992221-111401

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGAC**ATGAG**
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACACAGCTGGTGGTGTGTTCCC
TGTCAGAAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCA**GTAG**GGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAKVPKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGFILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RRLWVMPNHQVLLGPEEDQDHIYHPQ

0092321.11401

AGAAAGCTGCACCTCTGTTAGCTCCAGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACA**ATGA**ACCAACTCAGCTTCCTCTG
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTC
TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGCGCATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
ATGACTACAAGAACCCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAT
ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAACAGCATCTTATTACTCACCCATGGCCAGCGGGAATTCAGTCGGGGATT
TGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTGTGTGCTGGAATGAGG
TCACCGGATGTAACACTGAGCATCACTGATTTGGTGAGGAGGATACCTTCAGCAGGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATGGAGTGGATATGAAGTCACTGTTGGTTA
CAGCAGGACCGGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGT**TGA**GAGTTTTGTG
GAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDCEPSAFDGLYFLRTEN
 GVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGRWSSQQGSKADYPEGDGNWANYNTFG
 SAEATSDDYKNPGYYDIQAKDLGIWHVPNKS PMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
 YQKYPVKYGEKCTWTDNGPVPVIVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAAAN
 ALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
 CYR

FIGURE 297

GCGGAGCCGGCGCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCGGCATCCTGCCCTCGGAACAAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC
 ATGGGGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATAACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATAACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACACAACCTATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAAACAATATTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCATCTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCACTCTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACATAGATCTGAAGCATAATTTAAGAAAACATCAACATTTTTTG
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVADSSNTTVTMMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

09903521.111401

CACGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCCCAGCCGGGAGCGCCG
TCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGC**GATG**CGACCCCTGTGGGAGGC
CTTCTTGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCGTGCTGCTGCTGGC
GCAGCTGTCAGACGCGCCCAAGAATTTGAGGATGTCAGATGTAATGTATCTGCCCTCCCT
ATAAAGAAAAATCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
CATGTTGTGGAGCCCATGCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
ATGCAAATATGAAGAAAGAAGCTCTGTCAAA**TCAAGG**TTACCATTATAATTTATCTCTCCA
TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATCTACTGAAGAGG
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
TGCAAAATGCACAGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCAAAAGCTGTCTTTGACCGG
CATGTTGTCTCAGCT**TAA**TTGGGAATTGAACTCAAGTGACTAGAAAGAACAGGCAGCAAA
CTGGAAAGAACTGACTGGGTTTTGAGTGTTTCATTTAATACCTTGTGATTCTACCAACT
GTTGCTGGGAAGATCAAA**AACT**GGAAAGCAA**AACT**GTGCTGATTTTTTTTTCTGTTAACGTA
ATAATAGAGACATTTTTAA**AA**AGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTTG
TGACTTTTACTAATA**AAAA**TAAATCTGCCTGTAA**AT**TATCTTGAAGTCCTTTACCTGGAACA
AGCACTCTCTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
TTGTTGTTGTTTTTGTGTTGTTGTTTGGTGGGAGAGGGAGGGATGCCTGGGAAGTGGTT
AACA**AACT**TTTTTCAAGTCACTTTACTAA**CAAACT**TTTTGTAATAGACCTTACCTTCTATT
TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTG
ACTTTTGCACTGACTGATATATCTGGGAT**CT**GTGTGTCTGCACCTTCATGGTAAACGGGAT
CTAA**AAAT**GCCTGGTGGCTTTTCA**AAAA**AGCAGATTTTCTTCATGTA**CT**GTGATGTCTGATG
CAATGCATCCTAGAA**CAAACT**GGCCATTTGCTAGT**TTACT**CTAAAGACTAAACATAGTCTTG
GTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACA**AACT**CCTAAGGACTTGGACACT
TGCAATAAAGAAATTTTATTTTAAAGCCAGCCTCCCTGGATTGATAATATACACATTTG
TCAGCACTTCCGTCGTGGTGAAGGCACTGTTT**GAGCT**CCAATATGTGCAGCTTTGAACT
AGGCTGGGGTTGTGGGTGCCTCTTCTGA**AAAGTCT**TAACCATATTGGATAACTGGCTTTTTT
TCTTCTTATGTCCTCTTTTGAATGTAA**CAATAAAAAA**TAA**TTT**TGAAACATCAA

300/330

FIGURE 300

MATLWGGLRLGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS_{GH}IYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTII_{II}YLSILGLLLLY_{MY}VLTL
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
RKS_VFD_{RH}VVLS

0992521.11401
T04TT.1252660

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCCCAAGGCCTTCCTGTCCC GCGGAAGCGG
CAGGAGCCGCCGCCGACCTGAAGGAAAATTGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATGA[.]AAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAA[.]AACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCA[.]GTTCACATAAGAATG
TTTACTCAATGTTAAGTGT[.]TTTGCCCCAAAATTCACTAACAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTCTTAATCCAGTGAGTGATACAATTCAATGCAC[.]TCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLKAFLSRGKRQEPPTPEGKLGFRPPMMHHHQAPSDGQT
PGARFQ RSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPIYGFGLFYILYILFKVSRIILI
ILHQ

0000001 111101

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
 GGATTGAAAGTTGAGAGCAGCCATGTTTTTGCCCACTGAAACTCATCTGCTGCCAGTGTTAC
 TGGATTATTCCTGGGCCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTACGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTCCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCCTGACACTTGATGGGGGACATCTTATGC
 AATGATGGCTCTCTCCTGCTCCAAGATGTGAAGAGGCTGACCAGGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCCAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTTCGTTACTACCAAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTCAGCCCGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAAATCAGTTGGTGATCATTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
 GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTTTGAGGAAGTGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCCTGTGTGTGTCCTGGGCCACTCTACCACTGATTTCAGACTCCCGCTCTC
 CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTT
 GGATCAGACCCTCCTGTGGSCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAAATCAA

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
 GGATTGAAAGTTGAGAGCAGC

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTyceIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKL RMSVEYSQSWGHEFQNRVNLVGDIFRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIIGVIVCATILLLPVLILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEE PSEKSEATYMTMHPVWPSLR
SDRNN SLEKSGGGMPKTQQAF

0092521-11101

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
GGATGAAGATGGATACATCACCTTAATATTAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTGGGCTGGTGGCTCTGGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAAGCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAACAATCAGAACTAAAGGGCACTTCAAAGGTCATAATGCAGCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG
AGAACAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

0992221.11401

306/330

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSSWVRMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

0902521.111401

CCACACGCGTCCGCGCAGTCGCGCAGTTCTTGCTCCGCTGCCAGTCTCGCCCGCGATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACGCG
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCTTTGCTGAAGCCCGAGTGCGGAGAA
GCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGGAGACAGCGGACAAGCA
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**ATG**CGCGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGTCAGCAGCCCCAGCAAAGGCAAGACAGCTGC
GACAAAAACAAGTTAAATGCTTTTCCGGGTCAAACCTCTCGGCTCCAAGAAGAGCGCGAG
AAGAAGACCCAGAGCTCAGCTTGAAGGTATAGTTACCAAGCTATACAGCCGCAAGGCTACCC
ACTTGAAGCTGCAGCGGATGGAACCAATTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTCACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAATATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCGCAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAGAGGCAA
CCTATGTGAAGAGAACAAGCCTGCAGCTCATTTTCTGCCATAAACCATGAAAGTGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGTGAACGGAGGCAAATCCATGAGCCAGCTGAATCAAC
GTAGCCCAGTGAGGGCAAAGAAGGGCTCTGTAACGAGACCTTACCTCCAGTGCTGTTGAAT
TCTTCTAGCAGTCTTCAACCAAAGTCTCAATTTGATCAGCTTACCTATTACCAACCAACAGG
CAGAGTTCACTATTTCTATCGCCATTAGACCTCTTATCATPCATACCTACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVSFVKLFSGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTECKFKESVFENIYYVTYSSMIYRQQSGRGWYLGHNKEGIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAGGAAAAAACACCAAGGTTGGGTTCCTTCCTGACATTGGCAGTG
 CCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCACACCCTGTAGATTAC
 AAGAGTGGATTGTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAGGGGACGTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGCGGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGAGGTCCGCGAGCCCGGGGCGAGCCGGCCGTGTCCG
 CGCAGCGGGCGGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGTCTCCTATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCGCGCGGGCCGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCATTTCACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCCTGTCTCTTACCGCCAGCGTCGTCTTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTGATGAAGGGAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCGAGGCCTCCCTTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACCTCCAGTGAGCCAGCCACCACCAACCTGT

090224 111401

FIGURE 310

MAALASSLIQKREVREPGGSRPVSAQRRVCPRGTSKLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGI VTKLFCRQGFYLAQNPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRSGRAWYLGLDKEGQVMKGNR
VKKTAAAHLFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

310/330

ATGCGCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAGTGCATCTTCGGCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCAGCTCAAGGGTATAGTGACCAGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCACTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCTGAATGCAAGTT
TAAAGAATCTGTTTTGAAATATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACAGCAGCTATTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTCATGATGTTGGGCAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGGCTCTGCAATAATGAAATGGAGGCAACAGCTCAACAGAAGTAGACAAACATAG
G

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWD RPSASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRRLR
RQDPQLKGIVTRL YCRQGYLLQMHPD GALDGT KD DSTNSTL FNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

0002521 11401
10411 125260

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAAAT
 GAAGGATCGAGGACGCAGCTTTCTCTGGAAACCGAACCGAATGGATAAACTGATTGTGCAAGAGAGGAAGAA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGAGCATTCAAGAATG
 AATAAACCAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAAATAATATCTTAAAGCAGCTGTTCCC
 CTCGCCACCCCCAAAAAAGGATGATTGAAATGAAGAACCAGGAGGATTCACAAAGAAAAAGTATGTTCAATTT
 TTCTCTATAAAGGAGAAAGTGAGCCAAAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
 AGAAGCTGGTGGTGGTGGTCTTTCTTTCTTTTGAATTTCCACAAAGAGGAGAGGAAATTAATAATACATCTGC
 AAAGAAATTTTCAGAGAAGAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCCAGCAGAGCA
 CAGTTGGATTGTGCTATGTTGACTAAAAATGACGGATAATTGCAATTGGATTCTTCTCATCAACCTCCTTT
 TTTTAAATTTTTATTCTCTTTGGTATCAAGATCATGCGTTTCTCTTGTCTTAACCACTGGATTTCATCT
 GGATGTTGCTGTGATGCTGAAATACAACCTGTTGAATTCAGAAGGACCAACACCAGATAAATATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTTAGGTTTAACAGGGCCCTATTGACCCCT
 GCTTGGTGTCTGCTGGCTCTTCAACTCTTGTGGTGGTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGT
 GCTCTGCAGCAACCAAGTTGACGAAGGTGATTGTGTTCCGAAAAACCTGGTGGGTTCCGGATGGCATCTCC
 ACCAACACACAGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAGTGAACAGCTCTCAAGCACTTGAG
 GCACTTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCAATGAATTTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAATCTTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTTGATACCTGTGTCTAAA
 CTGAAGGAGCTCTGTTTGCAGAAACACCCCAATTGAAGCATCCCTTCTTATGCTTTTAACAGAATTCCTTCTTT
 GCGCGCATAGACTGTAGGGGAATTGAAAAGACTTTCATACATCTCAGAAGGTCCTTTGAAGGTCTGCGCAAT
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAG
 CTGGATCTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAACT
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGAATGCCTTTGACAACCTTCAGTCACTAGTGAGATCA
 ACCTGGCACACAATAACTATCAACTACTGCCTCATGACTCTTCACTCCCTTGATCATCTAGAGCGGATACAT
 TTACATCACAAACCTTGAACCTGTAACCTGTGACATCTGTGGCTCAGCTGGTGGATAAAAGACATGCCCCCTC
 GAACACAGCTTGTGTGCCGGGTGAACACTCCTCCCAATCTAAAGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTACATGCTATGCTCCGGTGATTGTGGAGCCCTCGACAGCTCAATGTCACTGAAGGATGGCAGCT
 GAGCTGAAATGTGCGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA
 TGGGGCGTCACAAGTGGCGGATAGCTGTGCTCAGTGATGCTTAAATTTACAACATGTAAGCTCGCAAGATA
 CAGGCATGTACACATGTATGGTGAGTAATCCGTTGGGAATACTACTGCTTCAGCCACCTGAAATGTACTGCA
 GCAACCACTACTCTTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGCAG
 GACCACAGATAACAATGTGGGTCCCCTCAGTGGTGCAGCTGGGAGACCACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAAGTCGACAGAAACCTTCAGCATCCAGTGACTGATATAACACAGTGGGATCGCAAGATA
 GATGAGGTGATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGACCATCGGCAAAACCATCAGCCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAGGCCACCTGCCCATGCTGTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAATCTCCCTTCAACCACACAACAGTTAAACACAATTAATCAATACA
 CAGTTCAGTGCATGAACCGTTATTGATCCGAATGAACCTCAAGACAATGTACAAGAGACTCAAATCTAAACA
 TTTACAGAGTTACAAAAACAACAATCAAAAAAAGACAGTTTATTAATAATGACACAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAAGTGCTTTACAAAAAACAAGAGAAAGAAATTTATTTATTAATAATCTATTG
 TGATCTAAAGCAGACAAAA

0903521-11101

FIGURE 314

MLNKMTLHPQQIMIGPRFNRLFDPLLVLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGISTNTRLNLHENQIQIIVNSFKHLRHLLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRDLGELKRLS
 YISEGAFEGLSNLRYNLAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTVDGTGMYTCMVSNSVGN
 TTASATLNVAATTPFSYFSTVTVETMEPSQDEARTDNNVGPFPVVDWETTNVTTSLTPQ
 STRSTEKTFTIPVTDINSIGIPGIDEVMKTKIIGCFVAITLMAAVMLVIFYKMRKQHRQN
 HHAPTRTVEIINVDDEITGDTFMESHLMPAIEHEHLNHYSYKSPFNHNTTNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCGGGGAGCCCATCTGCCCCCAGGGGACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCTGAGGCGCGCGCCAGCTCGCCCGAGGTCGGTCGGA
 GCGCGCCGCGCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
 GGGATGTCCTCCTCCTTCTCCTCTTGCTAGTTTCCCTACTATGTTGGAACTTGGGAACCTTGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTGGCCTGCCACCATTCACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGACAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAAAGTCTTAGTGAGACCATCCAAGCCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGAGTGATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGCTCGCTCCCAAATCTAGGATT
 GACTACAACCACCTTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTTACTCTGGACTGTA
 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCAGGTAAGTGTACAGT
 ATGTACAAGCATCGGCATGGTTGACAGGACATGACAGGCATAGTGGCTGGAGCCTGTCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAGAAAGATATGAGGAAGAGA
 GAGACCTAATGAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAACCCAGCT
 CCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTCTTCTCCTCCACTCGCTCCACAGCAAA
 AGTGCCTCAGCAGCCAGCGGACACTGTCAACTGACGCAGCAGCCCGAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACAAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCACACCCAGCATGATCCCGAGCCAGAGCAGAGCCTTCCAA
 ACGGCTGCAATTACAATGGACTTGACTCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACAGCCACACAACAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGACCGGAACAGATTGAGATGAGCATTTTCTTATACAATACCAACAGCAAA
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATGTGCCTTAGACAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTTGTTGACAGGACCTGTGGTGAGAAGGTTGGGGAAGGTTG
 AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTGTATCAGTGCTTTGATTACAATT
 TTAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAACTTATTGGATT
 ATTAGTTATTGACAGCTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGCTTCTTACTTGACTTAAC
 TTCAATTTGTATAAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTGTATTGAGCCCAAAATAAC
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCAAA
 CAGATGCCTCTAAGGACTTCTCTGCTAGATATTTCTGGAAGGAGAAAAACAACATGTCATT
 TATCAAGCTCCTTAGAAAGAAATCTTCTAGAGAAAAAGGATCTAGGAATGCTGAAAGATTA
 CCCAACATACCATTTATAGTCTCTTCTTCTGAGAAAATGTGAACCAAGATTTGAAGACTGG
 GTGGACTAGAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCGGCGGCA
 TGGTGGCAGGCCTGTAGGAAAATCCAGAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCATCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

0992521.1.1.101

316/330

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELETEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

0992521-111401

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCGCCTACCTGCAAGCCGCGGCCACGGCACGGCAGCCCA
 CCATGCGCGCTCCTGCTGCTGCTCTGCTCCTGTGCGGAGTAGTGGATTTCCGCCAGAAGTTTGAAGTATCACTACT
 CCTGAAGAGATGATTTGAAAAGGCCAAGGGGAACTGCCTATCTGCCATGCAAAATTTACGCTTAGTCCCGAAGA
 CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATTAATCAGAAGGTGGATCAAGTGATTTATTTAT
 ATTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAAGGCGGAGTACATTTTACAGGATATGATCT
 AATCTGGTGATGCATCAATTAATGTAAACGAATTTACAACGTGCAGATATTGGGCACATATCAGTGCAAAAGTGAA
 AAAAGCTCCTGGTGTGCAAAATGAAGAGATTCACTGGTAGTCTCTGTTAAAGCCTTCAGGTGCGAGATGTTACG
 TTGATGGATCTGAAGAAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTTCACTTCATTACAG
 TATGAGTGGCAAAAATTTGCTGACTCACGAAAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTAAAAAATGCTCTCTCGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCCTGTTGGCTCTAAACGTTGTCCCTCCTCAATAAAGCTGGACTAATTGACGAGGCCATTATAGGAAC
 TTGCTTGCTCTAGCGCTCATTGGTCTTATCATCTTTTCTGCTGCTGATAAAGCGCAGAGAGAAAAATATGAAAA
 GGAAGTTCATCAGATATCAGGGAAGATGTGCCACTCCAAAGAGCCGTACGTCCTATGCCAGAGCTACATCG
 GCAGTAATCATTCATCCCTGGGGTCCATGTCTCCTTCCACATGGAAGGATATCCAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACTCCTCAGAGTCCGACTCTCCACCTGCTAAGTCAAGTACCTTACAA
 GACTGATGGAATTACAGTTGTATATAATATGGACTACTGAAGATCTGAAGTATTGTATTATTTGACTTTATTTT
 AGGCCCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGAGCAGCTGTAAAGAACAC
 ATCTACTTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCATGTCAAATTTAGTACGAGCCAAATTCCTTGT
 TAAAAAACCCATGTATAGTGACACTGATAGTTAAAGAGTGTTTTATATATTTCAATAACTACCACTAACAA
 ATTTTTAACTTTTCATATGATATTTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTTCAA
 AGGAAATTTTAAATTTCTACGTTCTGTTTAAATGTTTTTGTCTATTTAGTTAAATACATTTGAAGGGAAATACCCG
 TTCTTTTCCCTTTTATGCACACAACAGAAACACGCGTTGTCATGCCTCAAACATATTTTATTTTGCAACTACA
 TGATTTTACACAAATTTCTTAAACAACGACATAAAATAGATTTCTTGTATATAAATAACTTACATACGCTCCA
 TAAAGTAAATTTCTCAAAGCTGTAGAACAATCGTCCACTTCTACAGTGTCTCGTATCCACAGAGTTGATGC
 ACAATATATAAATCACTCAGTCCAAATATTAATAAATTTAGGCACCTGACTAATCTTAAATAAATTTCTCAAACATA
 TATCAATATCTAAGTGCATATATTTTAAAGAAAGATTATTTCAATAAATCTATATAAATAAGTTTGTATGG
 TTGTGGCCCATCTAACTTCACTACTATTAGTAAGAACTTTTAACTTTTAAATGTGTAGTAAGGTTTATTTCTACCTT
 TTTCTCAACATGACACCAACACAATCAAAAACGAAGTTAGTGAGGTGCTAACTATGTGAGGATTAATCCAGTGAT
 TCCGGTCAACATGCATTCAGGAGGAGGTACCCATGTCACTGGAATTTGGGCGATATGGTTATTTTTTCTTCCC
 TGATTTGGATAACCAATTTGGAACAGGAGGAGGATAGTGATCTGATGGCCATTCCCTCGATACATTTCTGGCTT
 TTTCTGGGCAAAGGGTGCCACATTTGGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT
 TAAAGTTAATTCAAAGGAAAAATCATCATGTCTATGTTCCAGATTTCTCATTAAGACAAAAGTTACCCCAACACT
 GAGATCACTATCTAAGTGACATCTCTATTGTGAGTCTAAATACATTAACAACTCATGTATATAGCGGTATAA
 TGTATATCAAGGTGACCAATGTTTCTGAATGCATAAAGAAATGAATAAATCAACACAGTACTTCCATAACAA
 CTTCAACCAAAAAGACCAAAACATGGAACGAATGGAAGCTTTGAAGGACATGCTGTTGTTTATGCTAGTGGTTT
 CCACAGCTGGCTAGCCAGAGTCACTTGGAGCTTTTAAATCAAAAACATTTGAGCTGGAGGCTATTCCTT
 AGCAAACTAATGCAGAAACAGAAATCACTACCGCATGTTCTCACTTATAAGTGGGAGGTAAATGATAAGACT
 TATGACACAAGAGGAAAAACATAGACATTGAGCTATTTGACAGGGGAGGCTGGAGAGAGGAAAGGACGA
 GAAAGATAACTATTGAGTACTGCTTCAACCTGGGTGATGAATAATATGACACAAATCCCTGTGACACA
 TGTTTACCTATGGAACAACTCTCATGTGATCCCTAAACCTAAAATAAAGTTAAAAAATAAATAAATAA
 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

0993221 11401
 10111 123660

318/330

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
><subunit 1 of 1, 352 aa, 1 stop
><MW: 38938, pI: 7.86, NX(S/T): 3
MALLLCFVLLCGVVDFARSLSIITPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHVLVVKPSGARCYPVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLII FCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC
 CTCAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTGCG
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTGTCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTG
 CTTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAACTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC
 TTGTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGACACACAGCGGTTTCTGCTATTCCGGAGAGCATTCAAAAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGACATTCTTCTGACCTGGATGCAGAAATTTCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTCCCTGTGTCAATTCA
 AACAGTCTCCCTTCTCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGCTTACAGAGAAGATTCTTGATTTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACTGAACCTCAGAGCATGAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGTGCATCTGTTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCTTGGTGCCCTCCTTTTTTTTT
 TATCCTAGTCATCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGTCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
```

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLSWLTARFCPPLLATASQMOMVVLPCLGFTLLWSQVSGAQGQEFHFGPCQVK
 GVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVTLLLEFYLKTVEKNH
 HNRTEVVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
 TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

AAGGAGCAGCCCGCAAGCACCAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGACCATATAGAAGAGAGTTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCTGGCGTTTCTACGTGGACAGGGTGTTCAGGATCA
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACATATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGCTTTCTAGCCTGGATTAAATAAGAAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CATGCGTCTGGCCTCAGGCTGCTTATTGTCGCTTGAAAAATAGGCCAAAGTCTACTGTGGTAT
TTGTAAATAACTCTACTGTCTGCTGATATAGCCCTGCAGGCATCCTGGGAAGTAAGGGGTGCCTT
CCCATCTAATTATTATTGTAAGTCAATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATAACATACGATTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGCATGTTGGGGGCCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTGAC
CCGAGAACTGCAGGTTCACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
TCAGTATCACTTCTCGGTGAGTCTGGGCCGGGCGAAGAGAGCCTTCTGCCAGGCATGAACC
CACCCCGTACTCCAGTTCTGTCCCGAGGAACGAGATCCCCCTAATTCACCTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGCGGTCGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGGTCG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238
 ><subunit 1 of 1, 251 aa, 1 stop
 ><MW: 27954, pI: 9.22, NX(S/T): 1
 MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWGGLIHLTYTATARNSYHLQIHKNGHVD
 GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLNGY
 DVYHSPQYHFLVSLGRAKRAFLPGMNPPYSQFLSRNEIPLIHENTPIPRRHTRS AEDDSE
 RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
 KFI

Important features of the protein:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

090251-11407
 10411-1252660

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGC**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTCTGTCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCAGTGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCCTCTTCTAGGGCCTCAACCCAGCCGGCCCATTCAGAAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTG
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCTTTGCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCCTCTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTACAGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
 GTACAGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
 GGTCCCCGGGATCTGATGTCACTCTCTCTCGTGAAGCCCTGGTGACTGTCACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAACACACATCACTGAGGTACAGCCCTTGCCGAGACCCGTGTC
 ACAGCCGGCACCAAGAGTCACTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCTTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGAGTGGGCAAAACAACCTT
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGGCTCAAGAACCTCACCC
 CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGGACCTT
 CTTCTTCTGTCTCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGCGCCACCACAGACG**TGA**GTGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGTGAGTG
 TGGCTTCCCCGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAATCCACGCCACGCGCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGCGAGCATGTCCAAGCCCCAATCCCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTCACTGTTCAGAGGTTGCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCACTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCTGCA
 TTAATAATCACTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALQTLSA
ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSPNFMVLIATSVETSAASGSPEGAGM
TTVQGITGSDPEEAFPTDICTDSDSEAKLTMDILTLAHTSTEAKGLSSSESSASSDGPHPV
ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLEALVTVTN
EVINCSITEIETTTSSIPGASDIDLIPTIEGVKASSTSDPPALPDSTEAKPHITEVTSAAETL
STAGTTESAAPHAVTGTPLTNSATEREVPATGATTLGALVTSRNPLEETSALSVETPSY
VKVSGAAPVSEIAGSAGVKTTSTFAGSSANPTSEALKNFTPSETPTMDIATKGFPTSRD
PLPSVPPTTNSRGTNSTLAKITTSAKTTMKPOOPRRLPGRGRPOT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCGAGCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACCTAACTGAAATTTAAATGTTCTTCGGGGGAGAGGGGAG
 CTTGACTTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGCTCTAGAAGATGTTGTCTATTGACATCCAGTCTATCTCTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATCTTGTCTGTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAAGCA
 AAAAGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAACAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTTCAAAGCCCAACCGATATCTCATGGAGAGACACACTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGTACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTTCTGGGACTTCCAGCCACAGCTGCCCACACAGCTCCACCTGTAACACTGTCACTTCTC
 AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCTTA
 CTGCACTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCCAGAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGGTGATAGGCC
 TCGTCTCTGCGGTAGAACTCTTTCGGAATCACTCCGACAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGAAGCCCAATGCAATGAGTTTCTGCTGACTTGTAGTCTTAGCAGGAGTTG
 TATTTGAAAGACAGGAAAAATGCCCTTCTGCTTCTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGTTTCAACCTGTGTTGTGAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCCTCCTCGGCCCTCCCAAGTGCTGGGATTACAGG
 CATGAGCCACACAGCTGCCCCCTTCTGTTTTATGTTTTGGTTTTTGAGAAGGAATGAAGTG
 GGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAGTATAATTTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATCTTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTTCTTTTTATATGGATTCCCTTTAAACCTTATT
 CCAGATGTAGTCTCTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

0092521.11101

328/330

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVVIICFLTLRLSASQNCCLKKSLQEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKRTARQPCYLLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLP SQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEIHAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNLNTGNVYNPTALSMNSVESSTMNK TASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGTCTATGGGGTTGCCTGTCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGCTGTCTGGCACCATCTATGCAGAAAGAAAGGCGAGGACAAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTCTTCCAGGACCTGCTGTCTCCCTCCCTCTCTCCAC
 CTTCCAGCCTCTGGCTACAACAGCCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCACCCAGCGACCTCTCCTCTGACAGGGAGCTCCCGCCCCCTATGCAGC
 TGGACTCCACCTCAGCAGAGGACACAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCAGG
 GTGTCCATCCCGATGGTCCGCATCTGCCCCAGTCTGTGTCTGCTGAGCCTTCTGTGACG
 CGCAGCCCTGATCGCCTTCTGACGCCACCTGCTCCTGTGGAGAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAAAGTTCTGGCTCTCACGCTTGACTCGCGAGGAAAAGGAAGCC
 CCTTCCAGGCCCCGTAGGGGGACGTGATCTCGATGCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTGTCTCAGCGTAGGCGCAGGAGGCCCTCTGGCCAGGCCAGGAGT
 CAGCAGTATGGCTGGCTGGATCAGCACCGATTCCGGAAGGCTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTCCCCAGGCTCTCCTCTTGATGTTTCCA
 GCCTGACCTAGAACGCTTTGTGAGCCCTGGAGCCAGAGCGGTGGCCTTGCTCTTCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGCAGAGTACCAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC
 CTCATGCCAGTGTCGGACCCCTGCCTTCTCCCACTCCAGACCCCACTTGTCTTCCCTCCC
 TGGCGTCTCTCAGACTTAGTCCCAGGCTCTCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTGGCCCCACCAAGACCCCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACAATGCCAGTGACTGTGCACTTGAGTTTGGAGGCCAGTGGGCCCTG
 ATGAACGCTACACCCCTTACGCTTAGAGTCTGCATTGGGCTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGCTGCGACACCAGATCCACGTGGGACTCCCTGAGGCCCTGCTAAG
 TCCAGGCCCTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCCTTNCCTATTGGCCCTCCCTGGNCCATGCCTTCTGCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTGTCTGGAAGGGTTACTTGCCTATGGGTCTTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGGCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACCTATTTTTTTTCTTTTCCATTATTATTGTTTTTAAGACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGCACTGGCACGATCTGCAAACTCCGCCTCTGGGTTCAAGTGATT
 CTTCTGCCTCAGCCTCCGAGTAGTGGGATTACAGGCACGACCACCACCTGGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCCTGCTCTCAGTCTCCCAAAATGGCGGGATTACAGGATGAGCCACTGTG
 TCTGGCCCTATTTCTCTTAAAGTGAATTAAGAGTTGTTGATGATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGAAAAAATGTCAACCATAGTCTCACAGAGACTATCAT
 TATTTCGTTTGTGTGTTACTTCTTCCACTCTTTTCTTCTCACAATAATTGCGGGTGTCTT
 TTTACAGAGCAATATCTGTATATACAACCTTTGTATCTGCTTTTCCACCTTATCGTTCC
 ATCACTTTATTCCAGCACTTCTGTGTTTTACAGACCTTTTATAAATAAAATGTTTATCA
 GCTGCATAAAAAAAAAAAAAA

330/330

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAE EEGQETMKGRVSI RDSRQELSLIVTLWNLT LQDAGEYWC GVEKRGPD ESSLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG
TSQYGHERTS QYTGTS PHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFC SHLLLRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD
VISMPLHTSEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

0002521-44101